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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 17:57:26 ; Search time 698 Seconds  
(without alignments)  
9282.101 Million cell updates/sec

Title: US-10-016-647-1  
Perfect score: 1278  
Sequence: 1 atgactctggcgagcggg.....ccactgaattctctgaattaa 1278  
Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0  
Searched: 3340653 seqs, 2534793454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1278	100.0	1278	14	US-10-016-647-1
2	1278	100.0	1844	14	US-10-016-647-3
3	1276.4	99.9	3215	15	US-10-198-869-1
4	1178.4	92.2	2235	16	US-10-415-378-39
5	1099.4	86.0	1651	13	US-10-114-270-45
6	594	46.5	594	15	US-10-199-869-25
7	403.4	31.6	417	15	US-10-199-869-27
8	383	30.0	451	13	US-09-852-386-25
9	348.4	27.3	777	9	US-09-989-920-7
10	336.4	26.3	911	9	US-09-989-920-8
11	280	21.9	2370	10	US-09-971-392-139
12	277.4	21.7	2127	10	US-10-143-002-1
13	277.4	21.7	2127	15	US-10-325-891-1
14	260.6	20.4	3756	17	US-10-377-139-18

15	260.2	20.4	2565	13	US-10-435-935-10	Sequence 10, Appl
16	258.8	20.3	2022	17	US-10-738-455-18	Sequence 18, Appl
17	256	20.0	2499	15	US-10-101-510-628	Sequence 628, Appl
18	253.6	19.8	2882	17	US-10-377-139-19	Sequence 19, Appl
19	251	19.6	1518	17	US-10-738-455-2	Sequence 2, Appl
20	198.2	15.5	2483	14	US-10-143-002-3	Sequence 3, Appl
21	198.2	15.5	2483	15	US-10-325-891-3	Sequence 3, Appl
22	197.8	15.5	3102	15	US-10-121-746-17	Sequence 17, Appl
23	197.8	15.5	5027	15	US-10-101-510-439	Sequence 439, Appl
c	171	13.4	998	9	US-09-864-761-1804	Sequence 1804, Ap
25	171	13.4	1979	9	US-09-864-761-3784	Sequence 3784, Ap
26	166.2	13.0	1340	9	US-09-864-761-20550	Sequence 20550, A
27	157.4	12.3	3080	15	US-10-121-746-7	Sequence 7, Appl
28	151.8	11.9	1455	13	US-10-114-270-43	Sequence 43, Appl
29	151.6	11.9	1638	13	US-09-833-466-2	Sequence 2, Appl
30	151.6	11.9	1638	17	US-10-815-297-2	Sequence 2, Appl
31	151.6	11.9	2103	13	US-09-833-466-1	Sequence 1, Appl
32	151.6	11.9	2103	17	US-10-815-297-1	Sequence 1, Appl
33	151.2	11.8	1638	13	US-09-818-359-1	Sequence 1, Appl
34	151.2	11.8	2310	13	US-09-818-359-5	Sequence 5, Appl
35	150.4	11.8	2850	10	US-09-999-220B-1	Sequence 1, Appl
36	148.6	11.6	1871	10	US-09-999-220B-119	Sequence 119, App
37	148.6	11.6	2850	10	US-09-999-220B-115	Sequence 115, App
38	148.4	11.6	1871	10	US-09-999-220B-35	Sequence 35, Appl
39	146	11.4	1475	13	US-10-435-935-2	Sequence 2, Appl
40	146	11.4	2293	15	US-10-121-746-5	Sequence 5, Appl
41	146	11.4	2421	13	US-10-435-935-1	Sequence 1, Appl
42	145.4	11.4	1657	15	US-10-029-386-25090	Sequence 25090, A
c	143	11.2	763	15	US-10-029-386-24921	Sequence 24921, A
44	143	11.2	804	15	US-10-029-386-25062	Sequence 25062, A
45	141.6	11.1	2573	17	US-10-467-595-73	Sequence 73, Appl

## ALIGNMENTS

RESULT 1  
US-10-016-647-1  
; Sequence 1, Application US/10016647  
; Publication No. US00020160475A1  
; GENERAL INFORMATION:  
; APPLICANT: Hilbun, Carl Johan  
; APPLICANT: Hilbun, Erin  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide  
; FILE REFERENCE: LEX-0284-USA  
; CURRENT APPLICATION NUMBER: US/10/016,647  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/257,932  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1278  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-016-647-1

Query Match	100.0%;	Score 1278;	DB 14;	Length 1278;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1278;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGACCTTCGGGGCGAGCGGGCGGCTCGTGTGTGTGAACGTGGCGCGCCCGGTAT	60	
Db	1	ATGACCTTCGGGGCGAGCGGGCGGCTCGTGTGTGTGAACGTGGCGCGCCCGGTAT	60	
QY	61	TCGCTGTCCCGGAGCTGCTGAAGACTTCCGCTGCGCGCGCTGAGCGGCTCAGGC	120	
Db	61	TCGCTGTCCCGGAGCTGCTGAAGACTTCCGCTGCGCGCGCTGAGCGGCTCAGGC	120	
QY	121	TGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	180	
Db	121	TGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	180	

181 TACTTCTTCGACCGGCACTCGGAGGCTTCGGCTTCATCTGCTCTACGTGCGCGGCCAC 240  
 181 TACTTCTTCGACCGGCACTCGGAGGCTTCGGCTTCATCTGCTCTACGTGCGCGGCCAC 240  
 241 GGCAAGCTCGGCTTCGCGCGCGGAGTGGAGCTCTCTCTTACAAAGAGATGATCTAC 300  
 241 GGCAAGCTCGGCTTCGCGCGCGGAGTGGAGCTCTCTCTTACAAAGAGATGATCTAC 300  
 301 TGGGGCTGAGGCGGCACTTCGAGTACTGTCGAGCGCGCTTCGAGACCGCATG 360  
 301 TGGGGCTGAGGCGGCACTTCGAGTACTGTCGAGCGCGCTTCGAGACCGCATG 360  
 361 TCCGACACCTACACTTCTACTCGCGCGAGCGGCGTGTGGCGCGCGAGGCG 420  
 361 TCCGACACCTACACTTCTACTCGCGCGAGCGGCGTGTGGCGCGCGAGGCG 420  
 421 CGCGCGCGGCGGCGGCGGCTCCCTCCAGGGCTGGCTGGAGCGCATGCGCGGAC 480  
 421 CGCGCGCGGCGGCGGCGGCTCCCTCCAGGGCTGGCTGGAGCGCATGCGCGGAC 480  
 481 TTCGAGAGCGGCGGCTCGTGGCGCGAGATCCTGGCTAGCGTGTGGTGTTC 540  
 481 TTCGAGAGCGGCGGCTCGTGGCGCGAGATCCTGGCTAGCGTGTGGTGTTC 540  
 541 GTGATCGTGTCCATGTTGCTGTGGCGCGAGCGTTCGCGCGGCGGCGGCGG 600  
 541 GTGATCGTGTCCATGTTGCTGTGGCGCGAGCGTTCGCGCGGCGGCGGCGG 600  
 601 GCCGACACCGGCGGCGGAGCGGAGGATTAATGAAGCTATCTCATAGTTGG 660  
 601 GCCGACACCGGCGGCGGAGCGGAGGATTAATGAAGCTATCTCATAGTTGG 660  
 661 TTACTGCGGAGTGCATCGTGGTTCATTTCTCCAAAACAAGTGTGAGTTGCAAG 720  
 661 TTACTGCGGAGTGCATCGTGGTTCATTTCTCCAAAACAAGTGTGAGTTGCAAG 720  
 721 AGACCCCTGACATCATGATTTACTGGCAATCAGCGGCTATTACATCTGTGTTGAG 780  
 721 AGACCCCTGACATCATGATTTACTGGCAATCAGCGGCTATTACATCTGTGTTGAG 780  
 781 ACAGTGTTCACAGCGGAGACTCTCAACTCCAGAGGCTGGAGTCACTTTGAGGTA 840  
 781 ACAGTGTTCACAGCGGAGACTCTCAACTCCAGAGGCTGGAGTCACTTTGAGGTA 840  
 841 AGAATGATGAGGATTTTGGTGATTAAGCTTCGCGCTCACTTCATGTTCTCAGACA 900  
 841 AGAATGATGAGGATTTTGGTGATTAAGCTTCGCGCTCACTTCATGTTCTCAGACA 900  
 901 CTGGTTTGAATCTCAAAAGTTGCTACCGAGAGTGTGTTGTTGTTCTTCTTGT 960  
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 961 GTTCCCATGGAATCTTTAGTGCACTTTCTCAGCTTCTTGAAATGCGGCTGGAA 1020  
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 1141 GTTTGCTGTGCTAGTGAATGTTCTATGCGATTAATCTATCTTATCTACCATAGC 1200  
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 1201 TTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGACCTCTCC 1260  
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1261 ACTGAATTCCTGAATTA 1278  
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 RESULT 2  
 US-10-016-647-3  
 ; Sequence 3, Application US/10016647  
 ; Publication No. US20020160475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fiddle, Carl Johan  
 ; APPLICANT: Hilbun, Erin  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; TITLE OF INVENTION: NO. US20020160475A1 Human Ion Channel Protein and Polynucleotide  
 ; FILE REFERENCE: LEX-0284-USA  
 ; CURRENT APPLICATION NUMBER: US/10/016,647  
 ; CURRENT FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/257,932  
 ; PRIOR FILING DATE: 2000-12-20  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1844  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-10-016-647-3  
 Query Match 100.0%; Score 1278; DB 14; Length 1844;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGACCTTCGGCGCGGCGGCGGCTCGGTGCTGTGACGTGGCGGCGCGGAT 60  
 DB 457 ATGACCTTCGGCGCGGCGGCGGCGGCTCGGTGCTGTGACGTGGCGGCGGAT 516  
 QY 61 TCGCTGTCCCGGGAGCTCTGAAGACTTCCCGTGGCGCGGCTGAGCGGCTGACGGC 120  
 DB 517 TCGCTGTCCCGGGAGCTCTGAAGACTTCCCGTGGCGCGGCTGAGCGGCTGACGGC 576  
 QY 121 TCGCGCTCGAGCGGCGGAGTCTGAGGTGCGAGGACTACGACCGCGGCGGCAAGAG 180  
 DB 577 TCGCGCTCGAGCGGCGGAGTCTGAGGTGCGAGGACTACGACCGCGGCGGCAAGAG 636  
 QY 181 TACTTCTTCGACCGGCACTCGGAGGCTTCGGCTTCATCTGCTCTACGTGCGCGGCA 240  
 DB 637 TACTTCTTCGACCGGCACTCGGAGGCTTCGGCTTCATCTGCTCTACGTGCGCGGCA 696  
 QY 241 GGCAAGCTCGGCTTCGCGCGCGGAGTGTGAGGCTCTCTCTTCTACAAAGAGATGATCTAC 300  
 DB 697 GGCAAGCTCGGCTTCGCGCGCGGAGTGTGAGGCTCTCTCTTCTACAAAGAGATGATCTAC 756  
 QY 301 TGGGCGCTGGAGGCGGCGGCACTCGAGTACTGCTGCGAGCGCGGCTCGAGCGGCGATG 360  
 DB 757 TGGGCGCTGGAGGCGGCGGCACTCGAGTACTGCTGCGAGCGCGGCTCGAGCGGCGATG 816  
 QY 361 TCCGACACCTACACTTCTACTCGGCGGAGCGGCGGCTGCTGGCGCGGCGGAGCGG 420  
 DB 817 TCCGACACCTACACTTCTACTCGGCGGAGCGGCGGCTGCTGGCGCGGCGGAGCGG 876  
 QY 421 CGCGCGCGGCGGCGGCGGCGGCTCCCTCCAGGCGCTGGCTGGAGCGCATGCGCGGAGCC 480  
 DB 877 CGCGCGCGGCGGCGGCGGCGGCTCCCTCCAGGCGCTGGCTGGAGCGCATGCGCGGAGCC 936  
 QY 481 TTCGAGAGCGGCGGCGGCGGCTCGTGGCGCGGAGATCTTGGCTAGCGTGTGGTGGTTC 540  
 DB 937 TTCGAGAGCGGCGGCGGCGGCTCGTGGCGCGGAGATCTTGGCTAGCGTGTGGTGGTTC 996  
 QY 541 GTGATCGTGTTCATGAGTGTGCTGTGCGGCGGAGGCTGCGGCGGCGGCGGCGG 600  
 DB 997 GTGATCGTGTTCATGAGTGTGCTGTGCGGCGGAGGCTGCGGCGGCGGCGGCGG 1056  
 QY 601 GCCGACACCGGCGGCGGCGGCGGAGGAGGATAATTTGAAGCTATCTGATAGGTTGG 660







Db 1487 ACTACAGTGGCTATGAGATATGATCTATCTATCAGAGTGCCTGGAGGATTTCTGGAGGA 1546  
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Db 1547 GTTTGGTTGTCAGTGGAAATGTTCTATTGGCAATACCTATCATTATTTATCTACCATAGC 1606  
QY 1201 TTTGTCAGTGTATCATGAGCTCAAGTTTAGATTAGATCTGCTAGGTATAGTAG 1250  
Db 1607 TTTGTCAGTGTATCATGAGCTCAAGTTTAGATTAGATCTGCTAGGTATAGTAG 1656

RESULT 5

US-10-114-270-45  
; Sequence 45; Application US/10114270  
; Publication No. US20040030110A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Liu, Ziaohong  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Li, Li  
; APPLICANT: Vernst, Corine  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Smithson, Glenna  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Gangolli, Bsha A.  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Anderson, David W.  
; APPLICANT: Liette, Mario W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Stone, David J.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Rothenberg, Mark E.  
; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-322C  
; CURRENT APPLICATION NUMBER: US/10/114,270  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/281,086  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,020  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,930  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,512  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 470  
; SEQ ID NO 45

; LENGTH: 1651  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1642)  
US-10-114-270-45  
  
Query Match 86.0%; Score 1099.4; DB 13; Length 1651;  
Best Local Similarity 91.4%; Pred. No. 1.6e-309;  
Matches 1231; Conservative 0; Mismatches 11; Indels 105; Gaps 2;  
  
QY 1 ATGACCTTCGGCGCAGCGGGCGCTCGTGGTGTGTAACGTGGCGGCGCCCGGTAT 60  
Db 58 ATGACCTTCGGCGCAGCGGGCGGCTCGTGGTGTGTAACGTGGCGGCGCCCGGTAT 117  
QY 61 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCGGTGGCGCGGTGAGCCCGCTCAGCGC 120  
Db 118 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCGGTGGCGCGGTGAGCCCGCTCAGCGC 177  
QY 121 TCGCGCTCCGAGCGCGAGGTGCTCGAGGTGTGGAGCACTACGACCGCGAGCGCAACGAG 180  
Db 178 TCGCGCTCCGAGCGCGAGGTGCTCGAGGTGTGGAGCACTACGACCGCGAGCGCAACGAG 237  
QY 181 TACTTCTTCGACCGCGCACTCGAGGCGCTTCGGCTTCATCTCTCTACGTGGCGGCAC 240  
Db 238 TACTTCTTCGACCGCGCACTCGAGGCGCTTCGGCTTCATCTCTCTACGTGGCGGCAC 297  
QY 241 GCGAGCTGCGCTTCGGCGCGCGGATGTGGAGTCTCTCTCTTCTTACAGAGATGATCTAC 300  
Db 298 GCGAGCTGCGCTTCGGCGCGCGGATGTGGAGTCTCTCTCTTCTTACAGAGATGATCTAC 357  
QY 301 TGGGCGCTGGAGGCGCGCACTCGAGTACTGCTGCCAGCGCGCCCTCGACGACCGCATG 360  
Db 358 TGGGCGCTGGAGGCGCGCACTCGAGTACTGCTGCCAGCGCGCCCTCGACGACCGCATG 417  
QY 361 TCCGACACTACACTTTTACTCGGCCGAGCGAGCGGCGGTGCTGGGCGCGAGAGCG 420  
Db 418 TCCGACACTACACTTTTACTCGGCCGAGCGAGCGGCGGTGCTGGGCGCGAGAGCG 477  
QY 421 CGCGCGCGCGCGGCGGCTCCCTCCAGGCGGTGGCGGCGCATGGCGGACCTT 434  
Db 478 CGCGCGCGCGCGGCGGCTCCCTCCAGGCGGTGGCGGCGCATGGCGGACCTT 537  
QY 435 -----CGAGGCGGCTCCCTCCAGGCGGTGGCGGCGCATGGCGGACCTT 483  
Db 538 CGAGGAGCCACGCTCGCTGGCGCGAGGCGCTGGTGGAGCGCATGCGCGGACCTT 597  
QY 484 GAGGAGCCACGCTCGCTGGCGCGAGATCTCTGGCTAGCGGTGCGGTGGTGTG 543  
Db 598 GAGGAGCCACGCTCGCTGGCGCGAGATCTCTGGCTAGCGGTGCGGTGGTGTG 657  
QY 544 ATCGTGTCCATGGTGTGCTGTGGCGCAGCACGTTGCCCGACTGGCGCAACGCGAGCGCC 603  
Db 658 ATCGTGTCCATGGTGTGCTGTGGCGCAGCACGTTGCCCGACTGGCGCAACGCGAGCGCC 717  
QY 604 GACAAACGCGAGCTGGATGACCGGAG----- 629  
Db 718 GACAAACGCGAGCTGGATGACCGGAGTACTCCGCGCGCCCTGGGAGGAGCGCCCTCC 777  
QY 630 -----CAGGATATTAAGCTATTCGATAGGTGTTGTTCACTTCGCGAGTGC 675  
Db 778 GGGTGTTCCTTTGACAGGATTAATTAAGCTATTCGATAGGTGTTGTTCACTTCGCGAGTGC 837  
QY 676 ATCGTGAGGTTCATTGTCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACATC 735  
Db 838 ATCGTGAGGTTCATTGTCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACATC 897  
QY 736 ATGATTTTACTGGCAATCAGCGCGTATTACATCTCTGTGTTGATCAGAGTCTTTACAGCG 795  
Db 898 ATGATTTTACTGGCAATCAGCGCGTATTACATCTCTGTGTTGATCAGAGTCTTTACAGCG 957  
QY 796 GAGAACTCTCAACTCCAGAGGCGCTGGAGTCACTTGGGGTACTTTAGAAATGATGAGGATT 855

Db 958 GAGAACTCTCAACTCCAGAGGGCTGGAGTACCTTGAGGGTACTTGAATGATGAGGATT 1017  
 QY 856 TTTTGGGTGATTAAAGCTTGGCCGTCACCTTCAATGGTCTTCAGACACTCGGTTTGACTCTC 915  
 Db 1018 TTTTGGGTGATTAAAGCTTGGCCGTCACCTTCAATGGTCTTCAGACACTCGGTTTGACTCTC 1077  
 QY 916 AAACGTTGCTACCGAGAGATGGTTATGTTACTTGTCTTCAATTTGTGTGCCATGGCAATC 975  
 Db 1078 AAACGTTGCTACCGAGAGATGGTTATGTTACTTGTCTTCAATTTGTGTGCCATGGCAATC 1137  
 QY 976 TTTAGTGCACCTTCTCAGCTCTTGAACATGGCTGGACCTGGAACATCCACACAGGAC 1035  
 Db 1138 TTTAGTGCACCTTCTCAGCTCTTGAACATGGCTGGACCTGGAACATCCACACAGGAC 1197  
 QY 1036 TTTACCAAGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 1095  
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 QY 1096 GGAGATATGATCTCTATCAGTGCCTGGAGAAATCTTGGAGAGTTTGTGTGTCAGT 1155  
 Db 1258 GGAGATATGATCTCTATCAGTGCCTGGAGAAATCTTGGAGAGTTTGTGTGTCAGT 1317  
 QY 1156 GGAATTCCTTATTTGGCAATACCTATCATTCTTATCTACCATAGCTTTGTGTCAGTGTAT 1215  
 Db 1318 GGAATTCCTTATTTGGCAATACCTATCATTCTTATCTACCATAGCTTTGTGTCAGTGTAT 1377  
 QY 1216 CATGAGCTCAAGTTTAGATCTGTGAGG 1242  
 Db 1378 CATGAGCTCAAGTTTAGATCTGTGAGG 1404

RESULT 6

US-10-199-869-26  
 ; Sequence 26, Application US/10199869  
 ; Publication No. US20030152953A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
 ; FILE REFERENCE: D0161 NP  
 ; CURRENT APPLICATION NUMBER: US/10/199,869  
 ; CURRENT FILING DATE: 2002-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/306,577  
 ; PRIOR FILING DATE: 2001-07-19  
 ; NUMBER OF SEQ ID NOS: 90  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 26  
 ; LENGTH: 594  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-199-869-26

Query Match 46.5%; Score 594; DB 15; Length 594;  
 Best Local Similarity 100.0%; Pred. No. 28-162;  
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 634 ATAATTGAAGCTATCTGTCATAGTGTGGTTTCACTGCGGAGTGCATCGTGAAGTTTCAATTGTC 693  
 Db 1 ATAATTGAAGCTATCTGTCATAGTGTGGTTTCACTGCGGAGTGCATCGTGAAGTTTCAATTGTC 60  
 QY 694 TCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAAACATCATTTGATTTACTGGCAATC 753  
 Db 61 TCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAAACATCATTTGATTTACTGGCAATC 120  
 QY 754 ACCCGGTATTATACATCTCTGTGTTGATGACAGTGTTTTACAGGGGAGAACTCTCAATCCAG 813  
 Db 121 ACCCGGTATTATACATCTCTGTGTTGATGACAGTGTTTTACAGGGGAGAACTCTCAATCCAG 180  
 QY 814 AGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT 873  
 Db 181 AGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT 240

QY 874 GCCCGTCACTTCATTGTTGCTTTCAGACACTCGGTTTGAATCTCTCAACCGTTGCTACCGAGAG 933  
 Db 241 GCCCGTCACTTCATTGTTGCTTTCAGACACTCGGTTTGAATCTCTCAACCGTTGCTACCGAGAG 300  
 QY 934 ATGGTTATGTTACTTGTCTTCAATTTGTGTCATGGCAATCTTTAGTGCATTTCTTCAG 993  
 Db 301 ATGGTTATGTTACTTGTCTTCAATTTGTGTCATGGCAATCTTTAGTGCATTTCTTCAG 360  
 QY 994 CTTCTTGAACATGGGCTGGACCTGGAACATCCCAACAGGACTTTTACCAGCATTTCTCTGCT 1053  
 Db 361 CTTCTTGAACATGGGCTGGACCTGGAACATCCCAACAGGACTTTTACCAGCATTTCTCTGCT 420  
 QY 1054 GCCTGCTGGTGGTGAATTTCTTATGATACAGTGGCTATGAGATATGATATCTTATC 1113  
 Db 421 GCCTGCTGGTGGTGAATTTCTTATGATACAGTGGCTATGAGATATGATATCTTATC 480  
 QY 1114 ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTGTCAGTGGAAATTTTCTTATTTGGCA 1173  
 Db 481 ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTGTCAGTGGAAATTTTCTTATTTGGCA 540  
 QY 1174 TTACCTATCACTTTTATCTACCATAGCTTTTGTGTCAGTGGAAATTTTCTTATTTGGCA 1227  
 Db 541 TTACCTATCACTTTTATCTACCATAGCTTTTGTGTCAGTGGAAATTTTCTTATTTGGCA 594

RESULT 7

US-10-199-869-27  
 ; Sequence 27, Application US/10199869  
 ; Publication No. US20030152953A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
 ; FILE REFERENCE: D0161 NP  
 ; CURRENT APPLICATION NUMBER: US/10/199,869  
 ; CURRENT FILING DATE: 2002-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/306,577  
 ; PRIOR FILING DATE: 2001-07-19  
 ; NUMBER OF SEQ ID NOS: 90  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 27  
 ; LENGTH: 417  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-199-869-27

Query Match 31.6%; Score 403.4; DB 15; Length 417;  
 Best Local Similarity 99.3%; Pred. No. 6.28-107;  
 Matches 416; Conservative 0; Mismatches 1; Indels 2; Gaps 1;  
 QY 31 CTGGTGTGAAACGTGGGCGCGCCCGGTATTTCGCTGCCGCGAGCTGCTCAAGGACTTC 90  
 Db 1 CTGGTGTGAAACGTGGGCGCGCCCGGTATTTCGCTGCCGCGAGCTGCTCAAGGACTTC 60  
 QY 91 CCGCTGCGCGCGTGCAGCGGCTGCAGCGCTGCCGCTCCGAGCGCGAGCTGCTCGAGGTG 150  
 Db 61 CCGCTGCGCGCGTGCAGCGGCTGCAGCGCTGCCGCTCCGAGCGCGAGCTGCTCGAGGTG 120  
 QY 151 TGGCAGCACTACGACCCGCGAGCGCAACAGTACTTCTTCACCGGCACTCGGAGGCTTC 210  
 Db 121 TGGCAGCACTACGACCCGCGAGCGCAACAGTACTTCTTCACCGGCACTCGGAGGCTTC 180  
 QY 211 GGCTTCATCTCTGCTCTACGTGCGCGCCACGGAAGCTGCGCTTCGCGCGCGAGTGTGC 270  
 Db 181 GGCTTCATCTCTGCTCTACGTGCGCGCCACGGAAGCTGCGCTTCGCGCGCGAGTGTGC 240  
 QY 271 GAGCTCTCTTCTACACAGAGATGATCTACTGGGGCTGGAGGCGCGGCACTTCGAGTAC 330  
 Db 241 GAGCTCTCTTCTACACAGAGATGATCTACTGGGGCTGGAGGCGCGGCACTTCGAGTAC 300  
 QY 331 TGCTGCCAGCGCGCTTCGACGACCGCATCTCCGACCTACCTTCTACTCGGCGGAC 390  
 Db 301 TGCTGCCAGCGCGCTTCGACGACCGCATCTCCGACCTACCTTCTACTCGGCGGAC 360

Qy 391 GAGCCGGCGTGTGGCCGCGCAGAGGCGCGCCCGCGGGCGCCGAGCGGCTCCCTC 449

Db 361 GAGCCGGCGTGTGGCCGCGCAGAGGCGCGCCCGCGCG--CGAGCGGCTCCCTC 417

## RESULT 8

```

US-09-852-386-25
; Sequence 25, Application US/09852386
; Publication No. US20030064433A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00133_US1
; CURRENT APPLICATION NUMBER: US/09/852,386
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,305
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/207,092
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/206,526
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,033
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,093
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/216,893
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/237,873
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/223,245
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patent in version 3.0

```

```

; SEQ ID NO 25
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-386-25

```

Query Match	30.0%	Score 383;	DB 13;	Length 461;
Best Local Similarity	99.7%	Pred. No. 5.7e-101;		
Matches 394;	Conservative	0;	Mismatches 0;	Indels 1;
Gaps	1;			

Qy	885	CATTGGTCTTCAGACACCTCCGGTTTGACTCTCAACCGTTGGTACCCGAG-AGATGTTATGCT	943
Dp	1	CATTGGTCTTCAGACACCTCCGGTTTGACTCTCAACCGTTGGTACCCGAGAGATGTTATGCT	60

Qy	944	TACATTGCTTCATTTGTGTTGCCAATCTTTTAGTGCACCTTTCTCAGCTTCTTTGAAC	1003
Dh	61	TACTTTTGCTCCATTTGTGTTGCCAATCTTTTAGTGCACCTTTCTCAGCTTCTTTGAAC	120

Qy 1004 ATGGGCTGCACCTGGAAACATCCAAAGGACCTTTACCAAGCATTCCTGCTGCCTGCTGCT 1063

pb 121 ATGGGCTGGAACCTGGAAACATCCAAAGGACCTTTACCAAGCATTCCTGCTGCCTGCTGCT 180

Qy 1064 GGGTGATTATCTCTATGACTACAGTTGGCTATGGAGATATGTATCTTATCACAGTGCCTG 1123

bh 181 GGGTGATTATCTCTATGACTACAGTTGGCTATGGAGATATGTATCTTATCACAGTGCCTG 240

Qy 1124 GAAGAATCTTGGAGGAGTTGTGTGTGTCAGTGGAAATGTTCTATTGGCAATTACCTATCA 1183

[illegible]

QY 1244 ATAGTAGGAGCCTCTCCACTGAATTCCTGAATTAA 1278

Db : 361 ATAGTAGGAGCCTCTCCACTGAATTCCTGAATTAA 395

## RESULT 9

US-09-989-920-7/c  
; Sequence 7, Application US/09989920

```

; Patent No. US20020172957A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
;
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
;
; FILE REFERENCE: DEX-0291
;
; CURRENT APPLICATION NUMBER: US/09/989,920
;
; CURRENT FILING DATE: 2001-11-21
;
; PRIOR APPLICATION NUMBER: 60/252,500
;
; PRIOR FILING DATE: 2000-11-22
;
; NUMBER OF SEQ ID NOS: 284
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 7
;
; LENGTH: 777
;
; TYPE: DNA
;
; ORGANISM: Homo sapien
;
; US-09-989-920-7

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Query Match 27.3%; Score 348.4; DB 9; Length 777;  
Best Local Similarity 99.2%; Pred. No. 9e-91;  
Matches 371; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy	905	GTGTGACTCTCAAACGTTGCTACCGAGAGATGTTTAAGTTA	CATTGCTTCATTGTGTTG	964
Dh	703	GTGTGACTCTCAAACG-TGCTACCGAGAGATGTTTAAGTTAC-TGCTTCATTGTTGTTG		646

Qy	965	CCATGGCAATCTTTAGTGCATTTTCTCAGCTCTTTGACATGGCTGGACCTGGAAACAT	1024
pH	645	CCATGGCAATCTTTAGTGCATTTTCTCAGCTCTTTGACATGGCTGGACCTGGAAACAT	586

QY 1025 CCACCAAGGACTTTTACCAGCATTCCTGCTGCCTGCTGTGGGGTGATTATCTCTATGACTA 1084

D4 596 CCGCCATCAGCATTTTACCGAGCTTCCTGCTGCCTGCTGTGGGGTGATTATCTCTATGACTA 526

QY . 1085 CAGTTGGCTATGGAGATATGATCCTATCACACAGTGCCTGGGAATCTTGGAGGTTTT 1144

QY 1145 GTGTTGCAGTGGAAATTTCTATTGGCAATTACCTATCACTTTTATCCACCATAGCTTTG 12040

QY 1205 TGCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACTG 1266

QY 1265 AATTCTCGAATTAA 1278

## RESULTS

```

US-03-989-920-8
; Sequence 8, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920

```





Db 1712 CGACGGTGGGCTATGGGACATGGTCCCGAGAGCACCCCGGCGCAGGTAGTGGCCCTGA 1771  
 Qy 1142 TTGTGTTGTGTCAGTGGAAATGTTCTATTGGATACCTATACCTTTTATCTACCATAGCT 1201  
 Db 1772 GCAGCATCCTGAGCGGATCCTGCTCATGGCTTCCAGTCCAGTCCATCTTCCACACT 1831  
 Qy 1202 TTGTGAGTGTATCATGAGCTCAAG 1227  
 Db 1832 TCTCCCGCTCTTACCTGGAGCTCAAG 1857

## RESULT 12

US-10-143-002-1  
 ; Sequence 1, Application US/10143002  
 ; Publication No. US20020132775A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LI, ET AL.  
 ; TITLE OF INVENTION: Potassium Channel Protein 1  
 ; and 2

NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1

## CURRENT APPLICATION DATA:

US/10/143,002  
 FILING DATE: 13-May-2002

## CLASSIFICATION:

<Unknown>

## PRIOR APPLICATION DATA:

US/09/102,493

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/468,533

FILING DATE: 6 JUNE 1995

APPLICATION NUMBER: PCT/US94/08449

FILING DATE: 28 JUL 1994

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-310

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2127 BASE PAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-143-002-1

Query Match 21.7%; Score 277.4; DB 14; Length 2127;

Best Local Similarity 55.2%; Pred.No. 7.4e-70;

Matches 676; Conservative 0; Mismatches 501; Indels 48; Gaps 5;

Qy 38 TGAAGTGGCGGCGCGGCTATTGGCTGTCGCGGAGCTGCTGAAGGACTTCCCGCTGC 97

Db 481 TCAACGTAGCGGCATCAAGTACTCGCTGCCCTGGACCACTGGACGAGTTCCGCTGA 540

Qy 98 GCCCGGTGAGCGGCTGCACGCGCTCCGCTCGAGCGGACGCTGCTCGAGGTGTCGACG 157

Db 541 CGCGGCTGGCGGACGCTCAAGGCGCTGCACCACTTCGACGACATCTCAACGTCGCGATG 600

Qy 158 ACTACGACCGCGAGCGCAAGAGTACTTCTTCGACGGCACTCGGAGGCTTCGGCTTCA 217  
 Db 601 ACTACGACGTCACCTCAACAGAGTTCTTCTTCACGCAACCCGCGGCTTCGGCACTA 660  
 Qy 218 TCCTGTCTTACGTGCGCGGCAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCT 277  
 Db 661 TCTGTACCTTCTTGGCG---CGGGCAAGCTGCGGCTGCTGCGGAGATGTGCGCGCTGT 717  
 Qy 278 CTTTCTACAGAGATGATCTACTGGGGCTTGAGGGCGGCGACCTCGAGTACTTGTGCC 337  
 Db 718 CTTTCCAGGAGGAGCTGCTGTACTGGGGCATCGCGAGGACCACTTGGACGGCTGTGCA 777  
 Qy 338 AGCGCGCTCGACGACGCGCATGTCCGACACCTTACTCGCGCGACGACGCGG 397  
 Db 778 AGCGCGCTTACTGCGAGAGTTGAGAGTTCCGCGAGATGGTGGAGCGGAGAGAGG 837  
 Qy 398 GCCTGTGGCGCGGACGAGGCGCGCGCGGCGCGGCGCGAGGCGCGGCGCGGCGG 448  
 Db 838 ACGACGCTGGACAGCGAGGCGCGGACAGAGGCGCGCGCGGCGGCGGCGGCGGCGG 897  
 Qy 449 CCAGGCGCTGGCTGGAGCGCATCGCGGACCTTCGAGGAGCCACGTCGTCCTGSCCG 508  
 Db 898 TGGGGCGCTGCATGGCGGACTCGCGGACATGGTGGAGAGCGCGGCGGCTGCGCTG 957  
 Qy 509 CGCAGATCCTGGCTAGCGTGTGGTGTGTTCTGTGATCGTGTCCATGGTGTGCTGTGCG 568  
 Db 958 GCAAGGTGTTGCGCTGCTGTGCTGTGCTTCTGTGACCGTTCACCGCGCTCAACCTCTCG 1017  
 Qy 569 CCAGCAGTTGCCGACTGGCGCAAGCGAGCGCGGACCTTCGAGGAGCCACGTCGTCCTGSCCG 622  
 Db 1018 TCAGCACCTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1077  
 Qy 623 ACCGAGCAGGATAATTGAAGCTATCTGCATAGTGTGGTTCACCTGCGGAGTGCATGCTGA 682  
 Db 1078 ACAAGCTTTCATCGTGGAGTCGGTGTGCGTGGCTGGTTCCTCTGGAGTTCCTCTGCG 1137  
 Qy 683 GGTTCATTGTCTCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAGACATCATTTGATT 742  
 Db 1138 GGCTCATTCAGGCGCGGAGCAAGTTCGCTTCTCGGAGCGCGCTGACGCTGATCGACC 1197  
 Qy 743 TACTGGCAATCACGCGTATTACATCTCTGTGTTGATGACAGTGTTTACAGGCGAG--- 798  
 Db 1198 TGGTGGCAATCTGCGCTTACTATACGCTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1257  
 Qy 799 -----AACTCTCAACTCAGAGGCTGGAGTCACTTGGAGGTTACTTTA 841  
 Db 1258 GCAAGCGCGCGCGGCAACAGCTACTTGAACAAGGTGGGCTGGTGTGCGGCTGCTGC 1317  
 Qy 842 GAATGATGAGGATTTTGGTGTATTAAAGCTTGGCGTCACTTCACTTGTGCTTCAGACAC 901  
 Db 1318 GGGCGCTGCGCATCCTGTACGTGATGCGCTGGCGGCGCACTCCCTGGGCTGCGACGCG 1377  
 Qy 902 TCGGTTTGACTCTCAAAACGTTGCTACCGAGAGATGGTTATGTTACTTGTCTTCATTGTG 961  
 Db 1378 TGGGGCTACGCGCGCGCGCTGCACCGCGAGTTCGGGCTCCTGCTGCTTCTCTCTGCG 1437  
 Qy 962 TTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGCTGGAGCTGGAAA 1021  
 Db 1438 TGGCCATGCGCCCTTTCGCGCCCTGCTCTACGTCATCGAAGACGAGATGG----- 1488  
 Qy 1022 CATCCAAAGAGACTTTTACAGCATTCCTGCTGCCCTGCTGGTGGTGAATATCTCTATGA 1081  
 Db 1489 CCAGACCCCGAGTTCACGAGCATCCCTGCTGCTACTTGGTGGCTGTCATCACCATGA 1548  
 Qy 1082 CTACAGTTGGCTTAGGAGATATCTCTATACAGTGTCTGGAAGATTCCTTGGAGGAG 1141  
 Db 1549 CGACGGTGGACTATGGCGACATGGTCCAGAGGACCCCGGCGGAGTAGTGGCGCTGA 1608  
 Qy 1142 TTTGTGTGTGTCAGTGGAAATGTTCTATTGGCATTACTTCACTTCTTATCTACATAGCT 1201  
 Db 1609 GCAGCATCTGAGCGGATCCTGCTCATGCGCTTCCAGTTCACCTCATCTTCCACACT 1668

QY 1202 TTCTGAGTGTATCATGAGCTCAA 1226  
Db 1669 TCTCCCTCTCTACCTGGAGCTCAA 1693

RESULT 13

US-10-325-891-1  
; Sequence 1, Application US/10325891  
; Publication No. US2003092895A1  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: CARELLIA, BYRNE, BAIN, GILFILLAN,  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/325,891  
; FILING DATE: 23-Dec-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,492  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/464,340  
; FILING DATE: June 5, 1995

ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2127 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-325-891-1  
Query Match 21.7%; Score 277.4; DB 15; Length 2127;  
Best Local Similarity 55.2%; Pred. No. 7,4e-70;  
Matches 676; Conservative 0; Mismatches 501; Indels 48; Gaps 5;

QY 38 TGAACGTGGCGCGCCCGTATTCGCTCCCGGAGCTGCTGAAGACTTCCGCTGC 97  
Db 481 TCAACGTAGCGGCATCAAGTACTCGCTGCCCTGGACCACGCTGACGAGTTCGCGCTGA 540  
QY 98 GCGCGTGGAGCGGCTGACGCTGCGCTCCGAGCGGAGCTGCTCAGAGTGTCCGACG 157  
Db 541 CGGCGCTGGCCAGCTCAAGGCTGACCAATTGACGACATCTCAACGTTGCGATG 600  
QY 158 ACTAGACCGCGAGCGCAACGAGTACTTCTCGACCGGCACTTCGAGGCTTCGCTTCA 217  
Db 601 ACTAGACGCTCACTGCAACGAGTCTTCTCGACCGCAACCGCGGCGCTTCGCACTA 660  
QY 218 TCTGCTCTACGTGCGCGCCACGCAAGCTCGCTTCGCGCGCGGAGTGTCCGAGCTCT 277  
Db 661 TCTGACCTTCTGCGCG--CGGCAAGCTGCGCTGCTGCGCGAGATGCGCGCTGT 717  
QY 278 CCTTCTACAACGAGATGATCTACTGGGGCTTGGAGGCGCGCACCTCGAGTACTGCTGCC 337

Db 718 CCTTCCAGGAGAGCTCTGTACTTGGGCGCATTCGGGAGGACCACTTGGACGGTCTGTGA 777  
QY 338 AGCGCGCGCTCGACGACCGCATGTCCGACACCTACACCTTCTACTCGGCGCGAGCGG 397  
Db 778 AGCGCGCGCTACCTGCAAGATTGAGGAGTTCGGGAGATGGTGGAGCGGAGAGAGG 837  
QY 398 GCGTGTGGCGCGGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448  
Db 838 ACAGACGCGCTGAGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897  
QY 449 CCAGCGCTGCTGAGGCGCATTCGGGCGGACCTTCGAGGAGCGCACGCTCGCTCGCTGCGCG 508  
Db 898 TGGGCGCGCTGCAATGCGCGGACTGCGGACATGCTGGAGAGCGCGCATCGGGGCTGCTG 957  
QY 509 CGCAGATCCTGGCTAGCGTGTGCGTGTGCTGTGATCGTGTCCATGGTGGTGTGCTGCG 568  
Db 958 GCAAGGTGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017  
QY 569 CCAGCAGTTCGCGCGCTGCGGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 622  
Db 1018 TCAGCAGCTTGGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1077  
QY 623 ACCGAGCAGGATAATTGAAGCTATCTGCATAGGTTGGTTCACTGCGCGAGTGCATCGTA 682  
Db 1078 ARAAGTCTTCATGCTGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137  
QY 683 GGTTCATTGCTCCAAACAAAGTGTGAGTTTTCAGAGACCGCTGACACATCATTTGAT 742  
Db 1138 GGCTCATTGAGGCG 1197  
QY 743 TACTGGCAATCAGCGCGCTGATTTACATCTCTGTTGTATGACAGTGTGTTTACAGGCGAG 798  
Db 1198 TGGTGGCATCTGCGCTACTACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257  
QY 799 -----AACTCTCACTCAGAGGCTGAGTCACTTGGAGGTTACTTA 841  
Db 1258 GCAAGCG 1317  
QY 842 GAATGATGAGGATTTTGGTGTGATTAAGCTTCCCGTCACTTCACTTGGTCTTTCAGACAC 901  
Db 1318 GGGCGCTGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377  
QY 902 TCGTTTGACTCTCAACGCTGTACCGAGAGATGTTATGTTACTTGTCTTCACTTGTG 961  
Db 1378 TGGGCTCAGCG 1437  
QY 962 TTCCATGGCAATCTTTAGTGCATTTCTCAGCTTCTTGAACATGGCTGGACCTGGAA 1021  
Db 1438 TGGCATGCGCGCTTTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1488  
QY 1022 CATCCAAAGAGACTTTTACAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081  
Db 1489 CCGACAGCGCGAGTTCACCGAGCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548  
QY 1082 CTACAGTGTGCTATGAGATATGATTCCTATCAGAGCTGCTGGAAGAAATCTTGGAGGAG 1141  
Db 1549 CGAGCGTGGATATGCGGACATGCTCCCGAGGAGCACCGCGCGCGAGTAGTGGCGCTGA 1608  
QY 1142 TTTGTGTGTGCTGAGTGAATTTGTTCTATTGGCATTAACCTATCACTTTTATCTACCATAGCT 1201  
Db 1609 CGAGCATCTGAGGCGCATCTGCTCATGCGCTTCCAGTCACTTCCATCTTCCACACCT 1668  
QY 1202 TTGTGAGTGTATATGAGCTCAA 1226  
Db 1669 TCTCCCGCTCTACCTGGAGCTCAA 1693

RESULT 14  
US-10-377-139-18  
; Sequence 18, Application US/10377139  
; Publication No. US20040175761A1  
; GENERAL INFORMATION:

APPLICANT: Mackinnon, Roderick  
APPLICANT: Jiang, Youxing  
APPLICANT: Lee MacKinnon, Alice  
APPLICANT: Ruff, Vanessa  
TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins  
TITLE OF INVENTION: Uses Thereof  
FILE REFERENCE: Seq. Nos. 1-21 for 1119-9  
CURRENT APPLICATION NUMBER: US/10/377,139  
CURRENT FILING DATE: 2003-03-01  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 18  
LENGTH: 3756  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-377-139-18

Query Match 20.4%; Score 260.6; DB 17; Length 3756;  
Best Local Similarity 53.7%; Pred. No. 7,7e-65;  
Matches 645; Conservative 0; Mismatches 529; Indels 27; Gaps 4;

30 GGTGGTGTGTAACGTGGCGCGCGCGGTATTCGGTGTCCCGGGAGCTGTGAAGGACTT 89  
Db GGTCCGCTCAACGTTCGGGGGCTGGCGACGAGTACTCTGGCGTACCTCGGACCGGCT 319  
90 CCGGTGGCGCGGTGAGCGGCTGACGGTGGCGTCCGAGCGCGAGCTCGAGGT 149  
Db GCGCGCGCGCGGTGGGGAAGCTCCGCGACTGCAACAGCGACGACTCGCTCGAGGT 379  
150 GTGCGACGACTACGACCGCGCGCGCAAGAGTACTTCTTCACCGGCACTCGAGGCGTT 209  
Db GTGCGATGACTACAGCTCGACGACAGAGTACTTCTTCACCGGCACTCGAGGCGTT 439  
210 CGGCTTCTCTCTACAGAGATGATCTACTGGGCGCTGGAGGCGCGGCGGCTCGAGTA 269  
Db CACCTCCATC---CTCACTTACCGCACTGGCGGACTGCACATGATGGAGGAGATGTG 496  
270 CCAGCTCTCTCTACAGAGATGATCTACTGGGCGCTGGAGGCGCGGCGGCTCGAGTA 329  
Db CCGCTCAGCTTCAGCAGAGACTCGACTTGGGGCATCGACGAGATCACTCGAGTGC 556  
330 CTGCTGCCAGCGCGGCTCGACGAGCATGTTCGACACCTACACTTCTACTCGGCGCA 389  
Db CTGCTGCCAGCGCGGCTCGACGAGCATGTTCGACACCTACACTTCTACTCGGCGCA 607  
390 CGAGCGGCGGTGCTGGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 449  
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450 CAGGCGCTGGCTGGAGCGCATGGCGGCGACCTTCGAGGAGCGCGCGCGCGCGCGCG 509  
Db CGCAGAGAGAGGAGAGAGAACTCTGGGACCTACTGGAGAGCGCGCGCGCGCGCG 727  
510 GCGATCTGGCTGAGCGTGGTGTGTGATCGTGTGATCGTGTGATCGTGTGCTGTGCG 569  
Db CAAGATCTTGGCATATTTCCATCATGTTCATCGTTCCTTCCCATTTGGCGCTGTCC 787  
570 CAGCAGTTGCGCGA---CTGGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCG 626  
Db CAACAGCTGCTGAGCTACAGAGCTCGATGATTCGCGCGCGCGCGCGCGCGCGCG 847  
627 GAGCAGGATAATGAAGTATCTGATAGTGTGATGATGATGATGATGATGATGATGAT 686  
Db GCTGGCG 907  
687 CATTTGCTCCAAACAGGTGAGTTGTCAAGAGAGCGCGCGCGCGCGCGCGCGCGCG 746  
Db CCTCTCTCG 967  
747 GCGAATCAGCGCGGTATATATCTCTGTGTGATGACAGTGTGTACAGGCGGAACTCTCA 806  
Db GGCCATCTGCCATATATGTACCATTTTCTCCACCGAATTTCCACAGAGCGGTGTGCA 1027

## RESULT 15

US-10-435-935-10  
; Sequence 10, Application US/10435935  
; Publication No. US20040038890A1  
; GENERAL INFORMATION:  
; APPLICANT: Aiyar, Jayashree  
; Kang, Jiesheng  
; TITLE OF INVENTION: HUMAN VOLTAGE-GATED POTASSIUM  
; CHANNEL SUBUNIT  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZENECA Pharmaceuticals, Inc.  
; STREET: 1800 Concord Pike  
; CITY: Wilmington  
; STATE: DE  
; COUNTRY: USA  
; ZIP: 19850-5437  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/435,935  
; FILING DATE: 12-May-2003  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/074,878  
; FILING DATE: 08-MAY-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Higgins, Patrick H.  
; REGISTRATION NUMBER: 39,709  
; REFERENCE/DOCKET NUMBER: PHM.70310  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302.886.4889  
; TELEFAX: 302.886.8221  
; TELEX: <UNKNOWN>  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2565 base pairs

807 ACTCCAGAGGGCTGGAGTCACCTTGAGGTACTTAGAATGATGAGGATTTTGGTGAT 866  
Db ATTCCAGAAATGTCGCGCGGTGGTCCAGATCTTCCCATCATCGGAATTTCTCGCATCT 1087  
867 TAAGCTTTGCCCGTCACTTTCATTGGTCTTCAGACACTTCGGTTTGAATCTCAAAAGTTGCTA 926  
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987 TTCTCAGCTTCTTTGAACATGGGCTGGACCTCGAAACATCCAAACAGGACTTTTACACGAT 1046  
Db TGTCTTCTTGTCTGAGAGATGAGG-----CGACACCAAGTTCAAAAGCAT 1255  
1047 TCTGTGCTGCTGCTGGTGGTGAATATCTATGACTACAGTTGGTATGGAGATATGTA 1106  
Db CCCAGGCTCTTCTGGTGGGCCACCATCACCAGTACTGTGTGGTATGGAGATCTA 1315  
1107 TCTATCACAGTCCCTGGAGAAATCTTGGAGGAGTTTGTGTTCAGTGGAAATTTGTCT 1166  
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Db GATTGCTTCTCCATCCCATCATCGTCAATACTTCTCTGAGTTCTATAAGAGCAGAA 1435  
1227 G 1227  
Db 1436 G 1436

; TYPE: nucleic acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 us-10-435-935-10

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Matches 651;		Conservative 0;	Mismatches 523;	Indels 27;	Gaps 5;
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QY	90	CCCGCTCGCGCGGTGAGCCGGCTGCACGCTCCCGCTCCGAGCGGAGCTGCTCGAGGT	149		
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QY	210	CGGCTTCATCCTCTCTAGCTGGCGCGCCGCGCACGCAAGCTGGCTTCGCGCGCGGATGG	269		
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DB	321	CGCGCTCAGCTTCAGCAAGAGCTCGACTACTTGGGSCATCGACGAGATCTACTGGAGTC	380		
QY	330	CTGCTGGCAGCGCGCTCGACGACCGCATGTCCGACACCTACACCTTCTACTCGGCCGA	389		
DB	381	CTGCTGCCAGGCCCGCTTACCAC--CAGAAAGAGAGCAGATGAACGAGAGCTCAAGCGT	438		
QY	390	CGAGCGGGCGCTCTGGGCGCGGACGAGCGCGGCGCGCGCGCGCGCGCTCCCTC	449		
DB	439	GAGCGCGAGACTCTACGGGAGCGGAGAGCGGAG-----GAGTTCGATAACAGTGCTG	491		
QY	450	CAGCGCTGGTGGACGGCATGCGGGGACCTTCGAGGAGCCACGTCGTGCTGGCGGC	509		
DB	492	CGCAGAGAGAGGAAAAAATCTGGGACCTACTGGAGAGAGCCCAATTCCTCTGTGGCTGC	551		
QY	510	GCAGATCCTGGCTAGCGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	569		
DB	552	CAAGATCCTTGCATTAATTTCCATCATGTTCATGTCTCTCCACCATTTGCCCTGTCCCT	611		
QY	570	CAGCAGTTCGCCGA---CTGGCGCAACGACGCGCGCGCAACACCGAGCTGGATGACCG	626		
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QY	747	GGCAATCAGCGGTATTACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	806		
DB	792	GGCAATCTTGGCCATACTATGTACCATTTTCTCCGAAATCCAAAGAGCGTGTGTGCA	851		
QY	807	ACTCCAGAGGGTGGAGTCACTTGGAGTACTTAGAATGATGAGGATTTTGGGTGAT	866		
DB	852	ATTCCAGATGTCCGCGGCTGGTCCAGATCTTCGCAATCATGCGAATCTCCGCACTCT	911		
QY	867	TAAGCTTGGCGTCACTTCAATGGTCTTCAGACACTCGGTTTGACTCTCAAAAGTTGCTA	926		
DB	912	TAAGCTTGACGCCCACTCCACTGGGCTCCAGTCTCTGGGCTTCACTTTGGGAGAGCTA	971		
QY	927	CGGAGAGATGGTATGTACTTGTCTTCAATTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	986		

Search completed: October 6, 2004, 20:47:44  
 Job time : 707 secs

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QY	987	TTCTCAGCTTCTTTGAAACATGGGCTGGACCTGGAAACATCCAAAGGACTTTACCAGCAT	1046
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QY	1047	TCCTGCTCCCTGCTGGTGGGTGATTATCTATGACTACAGTTGGCTATGGAGATATGTA	1106
Db	1080	CCGAGCCTCTTCTGTGGTGGCCACCATCACCATGACTACTGTGGGTATGGAGACATCTA	1139
QY	1107	TCCTATCAGAGTGCCTGGAAGAATCTTGGAGGAGTTTGTGTGTGTGTGTGTGTGTGTGT	1166
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QY	1167	ATTGGCATTACCTATCACTTTTATCTACCATAGCTTTGTGCAGTGTATCATGAGTCAA	1226
Db	1200	GATTGCTCTTCCCATCCCATCATCTGCTCAATTAATCTCTCTGAGTTCTATTAAGGAGCA	1259
QY	1227	G 1227	
Db	1260	G 1260	

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 16:45:07 ; Search time 3656 Seconds  
(without alignments)  
10438.694 Million cell updates/sec

Title: US-10-016-647-1  
Perfect score: 1278  
Sequence: 1 atgaccttcggcgacgagcgg.....ccactgaattcctgaattaa 1278

Scoring table: OLIGO NUC  
Gapop'60.0 , Gapext 60.0  
Searched: 27513289 seqs, 14931090276 residues

Word size : 24  
Total number of hits satisfying chosen parameters: 19  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 45 summaries

Database : EST:\*  
1: em\_estba.\*  
2: em\_estbhm.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pin.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mas.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	152	11.9	500	28	AQ402619 HS 5066 A
C 2	115	9.0	385	28	AQ355274 CITR1-EI-
C 3	115	9.0	474	28	AQ354648 CITR1-EI-
C 4	104	8.1	301	29	CE495701 tigr-gss-

77	6.0	629	12	BM537928	BM537928 ha88c06.g
70	5.5	298	9	AI137172	AI137172 UI-R-C2p-
65	5.1	509	29	CG639652	CG639652 OST371309
50	3.9	166	29	CG513356	CG513356 OST66687
9	3.9	487	29	CG582101	CG582101 OST222985
10	3.8	484	29	CG662016	CG662016 OST444129
47	3.7	523	9	AI043703	AI043703 UI-R-CO-J
12	3.4	314	10	BF552004	BF552004 UI-R-C3p-
13	3.0	242	29	CG580684	CG580684 OST220291
14	3.0	499	28	AQ782780	AQ782780 HS 5301 A
15	2.7	262	29	CG661999	CG661999 OST444070
34	2.0	887	10	BF966122	BF966122 602286371
16	2.0	772	13	BU274588	BU274588 603533001
17	2.0	872	13	BU274588	BU274588 603533001
24	1.9	398	29	CG661991	CG661991 OST444030
24	1.9	487	29	CG604488	CG604488 OST280260

ALIGNMENTS

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LOCUS HS\_5066\_A2\_E01\_T7A RPCI-11 Human Male BAC Library Homo sapiens  
DEFINITION Genomic clone Plate=642 Col=2 Row=1, genomic survey sequence.  
ACCESSION AQ402619  
VERSION AQ402619.1 GI:4413531  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 500)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
PUBMED 10449764  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu  
plate: 642 row: 1 column: 2  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 500.  
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/note="vector: PBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the PBACe3.6 vector at EcoRI sites"

FEATURES  
source

3

ORIGIN

Query Match 11.9%; Score 152; DB 28; Length 500;  
Best Local Similarity 99.0%; Pred. No. 1.2e-65;  
Matches 302; Conservative 0; Mismatches 3; Indels

QY	878	GTCACTTCATTTGGTCTTCAGACACTCGGTTTGACTCTCAAACGTTGCTACCGAGAGATGG	937
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QY	938	TTATGTTACTTGTCTTCATTTGTGTTGCCATGGCAATCTTTAGTGCACCTTTCTCAGCTTC	997
Db	359	TTATGTTACTTGTCTTCATTTGTGTTGCCATGGCAATCTTTAGTGCACCTTTCTCAGCTTC	300
QY	998	TTGAACAATGGGCTGGACCTGGAACATCCAAACAAGGACTTTACGAGCAATTCCTGCTGCCT	1057
Db	299	TTGAACAATGGGCTGGACCTGGAACATCCAAACAAGGACTTTACGAGCAATTCCTGCTGCCT	240
QY	1058	GCTGGTGGGTGATTAATCTCTATGACTACAGTTGGCTATGGAGATATGTAATCTATCACAG	1117
Db	239	GCTGGTGGGTGATTAATCTCTATGACTACAGTTGGCTATGGAGATATGTAATCTATCACAG	180
QY	1118	TGCCTGGAGAATCTTGGAGGAGTTGTGTTCTGCAGTGGAAATGTTCTATTGGCAATTAC	1177
Db	179	TGCCTGGAGAATCTTGGAGGAGTTGTGTTCTGCAGTGGAAATGTTCTATTGGCAATTAC	120
QY	1178	CTATC 1182	
Db	119	CTATC 115	

RESULT 2	385 bp	DNA	linear	GSS 24-JAN-1999
ACQ355274				
LOCUS				
DEFINITION	CITBI-E1-2533B23.TP CITBI-E1 Homo sapiens genomic clone 2533B23, genomic survey sequence.			
ACCESSION	ACQ355274			
VERSION	ACQ355274.1	GI:4182447		
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 385)			
AUTHORS	Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.			
TITLE	Use of EAC End Sequences from CalTech Libraries for Sequence-Ready			

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JOURNAL
COMMENT
unpublished (1997)
Other_GSSs: CITBI-EI-2533B23.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

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Qy	1224	CAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAATTCCTGAATTA	1278	
Db	61	CAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAATTCCTGAATTA	115	

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LOCUS
DEFINITION
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    CITBI-E1-2533A24.TF CITBI-E1 Homo sapiens genomic clone 2533A24,
    genomic survey sequence.
ACCESSION
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VERSION
    AQ354648.1 GI:4181821
KEYWORDS
    GSS.
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 474)
    Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
    Venter,J.C.
TITLE
    Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
    Map Building
JOURNAL
    Unpublished (1997)
COMMENT
    Other GSSs: CITBI-E1-2533A24.TPB
    Contact: Shaying Zhao, William Nierman, Mark Adams
    Department of Eukaryotic Genomics
    The Institute for Genomic Research
    9712 Medical Center Dr., Rockville, MD 20850
    Tel: 301 838 0200
    Fax: 301 838 0208
    Email: hbs@igir.org
    Clones are available from Research Genetics (info@resgen.com). BAC
    end search page:
    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
    Seq primer: M13-21
    Class: BAC ends.

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Qy	1224	CAAGTTTATAGTCTGTAGGTATAGTAGAGGCTCTCCACTGAAATTCCTGGAATTA	1278		
Db	61	CAAGTTTATAGTCTGTAGGTATAGTAGAGGCTCTCCACTGAAATTCCTGGAATTA	115		

RESULT 4			
CE495701/c			
LOCUS			
CE495701	301 bp	DNA	linear
			GSS 28-SEP-2003



tigr-gas-dog-17000327301868 Dog Library Canis familiaris genomic,  
genomic survey sequence.  
CE495701 GI:36912482  
GSS.  
Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 301)  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
22875432  
14512627  
Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.  
Location/Qualifiers  
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/db\_xref="taxon:9615"  
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/note="Site1: BstXI; Libraries were prepared from  
peripheral blood"

ORIGIN  
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Best Local Similarity 99.08; Pred. No. 2.8e-41;  
Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 218 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGTGTGTGAACGTGGCGGGCCCCGGTAC 159  
QY 61 TCGGTGTCCGGGAGCTGCTGAAGAGACTCCCGTGGCGCGGTGAGCCGGCTGCACGGC 120  
Db 158 TCGGTGTCCGGGAGCTGCTGAAGAGACTTCCTCGGTGTGTGACCGCGGTGACCGGCTGCACGGC 99  
QY 121 TGCCTGTCCGAGCGCAGCTGCTCGAGGTGTGCGACGACTACGACCGCGACGGAACGAG 180  
Db 98 TGCCTGTCCGAGCGCAGCTGCTCGAGGTGTGCGACGACTACGACCGCGAGCGGAACGAG 39  
QY 181 TACTTCTTCGACCGGCACCTCGAGGC 206  
Db 38 TACTTCTTCGACCGGCACCTCGAGGC 13

RESULT 5  
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DEFINITION clone ha88c06 5', mRNA sequence.  
ACCESSION BM537928  
KEYWORDS BM537928.1 GI:18818563  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 629)  
O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Bailja,V.,  
Cunniss,D., Hedhja,N.N., de la Bastide,M., Katzenberger,F.,  
Muller,S., Nasrimento,I.U.

through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1787504  
Seq primer: M13 Forward  
POLYA-No.

## FEATURES

## source

Location/Qualifiers

1..298  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-C2p-oh-e-08-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-C2p"

/notes="vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C2p library is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6: 791-806, 1996)"

## ORIGIN

Query Match 5.5%; Score 70; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.5e-24;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 452 GCGCTGGCTGGAGCGATCGCGCGGACCTTCGAGGAGCCACGCTGCTGCGCGCGGC 511

Db 150 GCGCTGGCTGGAGCGATCGCGCGGACCTTCGAGGAGCCACGCTGCTGCGCGCGGC 91

QY 512 AGATCTGCG 521

Db 90 AGATCTGCG 81

## RESULT 7

## LOCUS

CG639652 509 bp DNA linear GSS 02-OCT-2003  
OST371309 Mus musculus 129Sv/Ev Mus musculus genomic clone  
OST371309, genomic survey sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 509)

## REFERENCE

## AUTHORS

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

## TITLE

## JOURNAL

## COMMENT

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene trap.  
Location/Qualifiers  
1..509  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST371309"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

## FEATURES

## source

Query Match 5.1%; Score 65; DB 29; Length 509;  
Best Local Similarity 100.0%; Pred. No. 2.2e-21;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 GCTGCTGCTGGTGGTGATTATCTCTATGACTACACTGGCTATGGATATGATCTCT 1110

Db 426 GCTGCTGCTGGTGGTGATTATCTCTATGACTACACTGGCTATGGATATGATCTCT 485

QY 1111 ATCAC 1115

Db 486 ATCAC 490

## RESULT 8

## LOCUS

CG513356 166 bp DNA linear GSS 01-OCT-2003  
OST66687 Mus musculus 129Sv/Ev Mus musculus genomic clone OST66687,  
genomic survey sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 166)

## REFERENCE

## AUTHORS

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com

## JOURNAL

## COMMENT

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene trap.  
Location/Qualifiers  
1..166  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST66687"

## FEATURES

## source

/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 3.9%; Score 50; DB 29; Length 166;  
Best Local Similarity 100.0%; Pred. No. 7.1e-14;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCTCCAAAACAAGTGTGAGTTGTCTCAAGAGACCCCTGAACATCATTTGA 740  
|||||  
DB 41 GTCTCCAAAACAAGTGTGAGTTGTCTCAAGAGACCCCTGAACATCATTTGA 90  
|||||

## RESULT 9

CG582101 487 bp DNA linear GSS 02-OCT-2003  
CG582101 Mus musculus 129Sv/Ev Mus musculus genomic clone  
DEFINITION OST222985, genomic survey sequence.

ACCESSION CG582101

VERSION CG582101.1 GI:37379484

## KEYWORDS

SOURCE GSS.

## ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS 1 (bases 1 to 487)  
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

## JOURNAL

COMMENT Contact: Zambrowicz BP

## FEATURES

source Location/Qualifiers

1..487  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 3.9%; Score 50; DB 29; Length 166;  
Best Local Similarity 100.0%; Pred. No. 9.5e-14;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 10

CG662016 484 bp DNA linear GSS 02-OCT-2003  
CG662016 Mus musculus 129Sv/Ev Mus musculus genomic clone  
DEFINITION OST444129 Mus musculus 129Sv/Ev Mus musculus genomic clone

ACCESSION OST444129

VERSION CG662016

KEYWORDS GSS.

## SOURCE

Mus musculus (house mouse)

QY 691 GTCTCCAAAACAAGTGTGAGTTGTCTCAAGAGACCCCTGAACATCATTTGA 740  
|||||  
DB 56 GTCTCCAAAACAAGTGTGAGTTGTCTCAAGAGACCCCTGAACATCATTTGA 105  
|||||

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 484)  
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.

## TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

## JOURNAL

## COMMENT

Contact: Zambrowicz BP

## FEATURES

## source

Location/Qualifiers  
1..484  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 3.8%; Score 49; DB 29; Length 484;  
Best Local Similarity 100.0%; Pred. No. 3.1e-13;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

691 GTCTCCAAAACAAGTGTGAGTTGTCTCAAGAGACCCCTGAACATCATTTG 739  
|||||

## DB

65 GTCTCCAAAACAAGTGTGAGTTGTCTCAAGAGACCCCTGAACATCATTTG 113  
|||||

## RESULT 11

AI043703 523 bp mRNA linear EST 05-JUL-1999  
LOCUS UI-R-CO-31-g-04-0-UI.s1 UI-R-CO Rattus norvegicus cDNA clone  
DEFINITION UI-R-CO-31-g-04-0-UI 3', mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE

## AUTHORS

## TITLE

1 (bases 1 to 523)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Genome Res. 6 (3), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bento-soares@uiowa.edu  
Oligo-dt track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.  
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available  
through Research Genetics This clone is also available through the

I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE  
 ID=1783128  
 Seq primer: M13 Forward  
 FOLDIA=No.

## FEATURES

## Location/Qualifiers

1. 523  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-C0-j1-g-04-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-C0"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-Al and UI-R-E1 libraries. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-Al and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

## ORIGIN

Query Match 3.7%; Score 47; DB 9; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 691 GTCTCAAAACCAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCAT 737  
 DB 96 GTCTCAAAACCAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCAT 142

## RESULT 12

## BF552004

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

BF552004 314 bp mRNA linear EST 12-DEC-2000  
 UI-R-C2p-of-h-09-0-UI.r1 UI-R-C2p Rattus norvegicus cDNA clone  
 UI-R-C2p-of-h-09-0-UI 5', mRNA sequence.  
 BF552004  
 BF552004.1 GI:11661734  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 314)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 8889548  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics (www.resgen.com)  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL (info@image.llnl.gov). IMAGE ID= 178420 The following  
 repetitive elements were found in this cDNA sequence: 97-157,  
 >GC rich#Low complexity

## FEATURES

## Location/Qualifiers

1. 314  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-C2p-of-h-09-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-C2p"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-C2p library is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

## ORIGIN

Query Match 3.4%; Score 43; DB 10; Length 314;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-10;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GC GGCGCGGCTCGTGTGCTGAACTGGCGGCGCGCCCGTA 59  
 DB 147 GC GGCGCGGCTCGTGTGCTGAACTGGCGGCGCGCCCGTA 189

## RESULT 13

## CG580684

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

CG580684 242 bp DNA linear GSS 02-OCT-2003  
 OST220291 Mus musculus 129Sv/Ev Mus musculus genomic clone  
 OST220291, genomic survey sequence.  
 CG580684  
 CG580684.1 GI:37376130  
 GSS.  
 Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 242)  
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
 Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J.J., Finch, R.A.,  
 Priddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
 Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,  
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
 Zhu,Q., Person,C. and Sands,A.T.  
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.

## FEATURES

source  
 1. .242  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="129SV/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST220291"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129SV/Ev"

## ORIGIN

Query Match 3.0%; Score 38; DB 29; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 1e-07;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CTTGAACATGGCTGGACCTCGAACATCCACACAGGA 1034  
 |||||  
 DB 103 CTTGAACATGGCTGGACCTCGAACATCCACACAGGA 140

## RESULT 14

AQ782780 499 bp DNA linear GSS 02-AUG-1999  
 LOCUS HS 5301 Al E04 T7A RPT-11 Human Male BAC Library Homo sapiens  
 DEFINITION genomic\_clone Plate=877 Col=7 Row=I, genomic survey sequence.

ACCESSION AQ782780  
 VERSION AQ782780.1 GI:5685740  
 KEYWORDS GSS.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 499)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 PUBMED 10449764

## COMMENT

Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPT-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
 or from Research Genetics (info@resgen.com). BAC end Web Server:  
 http://www.htsc.washington.edu  
 Plate: 877 row: I column: 7  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 499.

## FEATURES

source  
 1. .499  
 Location/Qualifiers

/organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="plate=877 Col=7 Row=I"  
 /sex="male"  
 /clone\_lib="RPT-11 Human Male BAC Library"  
 /note="Vector: pBACe3.6; Site1: EcoRI; Site2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACe3.6 vector at EcoRI sites"

## ORIGIN

Query Match 3.0%; Score 38; DB 28; Length 499;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1162 GTTCTATTGGCATTACCTATCACTTTTATCTACCATAG 1199  
 |||||  
 DB 54 GTTCTATTGGCATTACCTATCACTTTTATCTACCATAG 91

## RESULT 15

CG661999 262 bp DNA linear GSS 02-OCT-2003  
 LOCUS OST444070 Mus musculus 129SV/Ev Mus musculus genomic clone  
 DEFINITION OST444070, genomic survey sequence.

ACCESSION CG661999  
 VERSION CG661999.1 GI:37485848  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 262)

AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
 Piggett,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
 Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
 Zhu,Q., Person,C. and Sands,A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 COMMENT Contact: Zambrowicz BP

## JOURNAL

OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.

## FEATURES

source  
 1. .262  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="129SV/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST444070"  
 /call\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129SV/Ev"

## ORIGIN

Query Match 2.7%; Score 34; DB 29; Length 262;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 TTACAGGCGAGAACTCTCAACTCCAGAGGCTGG 821  
 |||||  
 DB 110 TTACAGGCGAGAACTCTCAACTCCAGAGGCTGG 143

Thu Oct 7 10:52:17 2004

us-10-016-647-1.oligo.rst

Page 8

Search completed: April 19, 2004, 19:32:52  
Job time : 3663 secs







QY 1021 ACATCCAAACAGGACTTTACAGGATTCCTGCTGCTGCTGGTGATTTCTCTATG 1080  
 Db 1477 ACATCCAAACAGGACTTTACAGGATTCCTGCTGCTGCTGGTGATTTCTCTATG 1536  
 QY 1081 ACTACAGTTGGCTATGGAGATATGATCTATCAAGTGCCTGGAGAAATCTTTGGAGGA 1140  
 Db 1537 ACTACAGTTGGCTATGGAGATATGATCTATCAAGTGCCTGGAGAAATCTTTGGAGGA 1596  
 QY 1141 GTTGTGTGTGTCAGTGGAAATGTTCTATTTGGCAATACCTATCACTTTTATCTACCATAGC 1200  
 Db 1597 GTTGTGTGTGTCAGTGGAAATGTTCTATTTGGCAATACCTATCACTTTTATCTACCATAGC 1656  
 QY 1201 TTTGTGCAAGTTTATCATGAGCTCAAGTTTAGATCTGCTAGTATAGTATAGGAGGCTCTCC 1260  
 Db 1657 TTTGTGCAAGTTTATCATGAGCTCAAGTTTAGATCTGCTAGTATAGTATAGGAGGCTCTCC 1716  
 QY 1261 ACTGAATTCCTGAATTA 1278  
 Db 1717 ACTGAATTCCTGAATTA 1734

RESULT 3  
 US-10-199-869-1  
 ; Sequence 1, Application US/10199869  
 ; Publication No. US20030152953A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
 ; TITLE OF INVENTION: K-alpha2  
 ; FILE REFERENCE: D0161 NP  
 ; CURRENT APPLICATION NUMBER: US/10/199,869  
 ; CURRENT FILING DATE: 2002-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/306,577  
 ; PRIOR FILING DATE: 2001-07-19  
 ; NUMBER OF SEQ ID NOS: 90  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 3215  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1275)  
 ; OTHER INFORMATION:  
 US-10-199-869-1

Query Match 96.0%; Score 1227; DB 15; Length 3215;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 181 TACTTCTTCGACCGGCACTCGGAGGCTTCGGCTTCATCTGCTCTACGTCGCGGCGCAC 240  
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 QY 421 CGCGCGCGCGCGCGCGAGCGGCTCCCTCGAGCGGCTGCTGAGCGGCTGCGCGCGAGCG 480  
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 QY 541 GTGATCGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 Db 541 GTGATCGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 QY 601 GCGGACAAACCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 Db 601 GCGGACAAACCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 661 TTTCACTGCCGAGTGCATCGTGAAGTTTCATTTCTCCAAAAACAAGTGTGATTTGCTCAAG 720  
 Db 661 TTTCACTGCCGAGTGCATCGTGAAGTTTCATTTCTCCAAAAACAAGTGTGATTTGCTCAAG 720  
 QY 721 AGACCCCTGAACATCATTTACTGGCAATCAGCGCGTATTACATCTCTGCTGCTGCTGCTG 780  
 Db 721 AGACCCCTGAACATCATTTACTGGCAATCAGCGCGTATTACATCTCTGCTGCTGCTGCTG 780  
 QY 781 ACAGTGTTCACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTTGAGGCTACTT 840  
 Db 781 ACAGTGTTCACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTTGAGGCTACTT 840  
 QY 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTTCAGCTTTCAGCTTTCAGCTTTCAGATA 900  
 Db 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTTCAGCTTTCAGCTTTCAGCTTTCAGATA 900  
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 QY 1261 ACTGAATTCCTGAATTA 1278  
 Db 1261 ACTGAATTCCTGAATTA 1278

RESULT 4  
 US-10-415-378-39  
 ; Sequence 39, Application US/10415378  
 ; Publication No. US20040014945A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom  
 ; APPLICANT: YUE, Henry; NGUYEN, Damiel B.;

```

; APPLICANT: HAPALIA, April J.A.; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
; APPLICANT: GANDHI, Ameena R.; DING, Li;
; APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
; APPLICANT: ARVIZU, Chandra S.; GIETZEN, Kimberly J.;
; APPLICANT: KHAU, Preeti G.; AZIMZAI, Yalda;
; APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;
; APPLICANT: THORNTON, Michael B.; LU, Dying Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
; APPLICANT: ISON, H. Craig; DAS, Debopriya;
; APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0270 USN
; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,661
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040014945A1 7482060CB3
; US-10-415-378-39

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Query Match	57.0%;	Score 729;	DB 16;	Length 2235;
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QY	574	ACGTTGCCGACTGGCGCAACAGCAGCGCGCGCAACCGCAGCTGGATTCACCGGACGAGG	633	
Db	980	ACGTTGCCGACTGGCGCAACAGCAGCGCGCGCAACCGCAGCTGGATTCACCGGACGAGG	1039	
QY	634	ATAATTGAGACTATCTGCATAGGTTGGTTCACTGCCGAGTCGATCGAGGTTCAATTGTC	693	
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Db	1100	TCCAAAACAAGTGTGAGTTGTTCAAGAGACCCCTGAACATCATTGATTTATCGCAATC	1159	
QY	754	ACGCCGATTACATCTCTGTGTTGATGCAGAGTGTTCAGGGCAGAAGCTCTCAACTCCAG	813	
Db	1160	ACGCCGATTACATCTCTGTGTTGATGCAGAGTGTTCAGGGCAGAAGCTCTCAACTCCAG	1219	
QY	814	AGGCGTGGAGTCACCTTGAGGGTACTTAGAATGATGAGATTTTTTGGGTGATTAAAGCTT	873	
Db	1220	AGGCGTGGAGTCACCTTGAGGGTACTTAGAATGATGAGATTTTTTGGGTGATTAAAGCTT	1279	
QY	874	GCCCGTCACTTCATTGGTCTTTAGACACCTCGCGTTTGACTCTCAAAACGTTGCTACCGAGAG	933	
Db	1280	GCCCGTCACTTCATTGGTCTTTAGACACCTCGCGTTTGACTCTCAAAACGTTGCTACCGAGAG	1339	

## RESULT 5

US-10-114-270-45

Sequence 45, Application US/10114270  
Publication No. US20040030110A1  
GENERAL INFORMATION:  
APPLICANT: Guo, Xiaojia  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Miller, Charles E.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Spytak, Kimberly A.  
APPLICANT: Patturajan, Meera  
APPLICANT: Liu, Zhaozhong  
APPLICANT: Gusev, Vladimir Y.  
APPLICANT: Li, Li  
APPLICANT: Vernet, Corine  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Gorman, Linda  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Smithson, Glennda  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Gangolli, Esha A.  
APPLICANT: Taupier Jr., Raymond J.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Ji, Weizhen  
APPLICANT: Anderson, David W.  
APPLICANT: Lietz, Mario W.  
APPLICANT: Rastelli, Luca  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Stone, David J.  
APPLICANT: MacDougall, John B.  
APPLICANT: Rothenberg, Mark E.  
TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encodings  
FILE REFERENCE: 21402-322C  
CURRENT APPLICATION NUMBER: US/10/114,270  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/281,086  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05

;; PRIOR APPLICATION NUMBER: 60/282,020  
;; PRIOR FILING DATE: 2001-04-06  
;; PRIOR APPLICATION NUMBER: 60/282,930  
;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/282,934  
;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,512  
;; PRIOR FILING DATE: 2001-04-12  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 470  
;; SEQ ID NO 45  
;; LENGTH: 1651  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(1642)  
US-10-114-270-45

Query Match 48.0%; Score 613; DB 13; Length 1651;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 690 TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACAATGATTGTTACTGGC 749  
Db 852 TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACAATGATTGTTACTGGC 911  
  
QY 750 AATCAGCCGCTATACATCTCTGTGTGATGACAGTGTTCAGGCGGAACTCTCAACT 809  
Db 912 AATCAGCCGCTATACATCTCTGTGTGATGACAGTGTTCAGGCGGAACTCTCAACT 971  
  
QY 810 CCAGAGGGCTGGAGTCACTTGAAGGTACTTAGAATGATGAGATTTTGGGTGATTAA 869  
Db 972 CCAGAGGGCTGGAGTCACTTGAAGGTACTTAGAATGATGAGATTTTGGGTGATTAA 1031  
  
QY 870 GCTTGCCCGTCACTTCACTGTTCTTCAGACACTCGGTTGACTCTCAACGTTGCTACCG 929  
Db 1032 GCTTGCCCGTCACTTCACTGTTCTTCAGACACTCGGTTGACTCTCAACGTTGCTACCG 1091  
  
QY 930 AGAGATGGTTATGTTACTTCTTCACTTGTGTGCTATGGCAATCTTTAGTGCATTTTC 989  
Db 1092 AGAGATGGTTATGTTACTTCTTCACTTGTGTGCTATGGCAATCTTTAGTGCATTTTC 1151  
  
QY 990 TCAGCTTCTTGAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTTACAGCAATTC 1049  
Db 1152 TCAGCTTCTTGAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTTACAGCAATTC 1211  
  
QY 1050 TGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGGAGATATGATCC 1109  
Db 1212 TGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGGAGATATGATCC 1271  
  
QY 1110 TATCACAGTCCCTGGAAAGAAATCTTGGAGAGATTTGTGTGTCAGTGGAAATGTTCTATT 1169  
Db 1272 TATCACAGTCCCTGGAAAGAAATCTTGGAGAGATTTGTGTGTCAGTGGAAATGTTCTATT 1331  
  
QY 1170 GGCATTACCTATCACTTTTATCACCATAGCTTTGTGTCAGTGTATCATGAGCTCAAGTT 1229  
Db 1332 GGCATTACCTATCACTTTTATCACCATAGCTTTGTGTCAGTGTATCATGAGCTCAAGTT 1391  
  
QY 1230 TAGATCTGCTAGG 1242  
Db 1392 TAGATCTGCTAGG 1404

RESULT 6

US-10-199-869-26  
;; Sequence 26, Application US/10199869  
;; Publication No. US20030152953A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bristol-Myers Squibb Company  
;; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
;; FILE REFERENCE: D0161 NP  
;; CURRENT APPLICATION NUMBER: US/10/199,869  
;; PRIOR FILING DATE: 2002-07-19  
;; PRIOR APPLICATION NUMBER: US 60/306,577  
;; PRIOR FILING DATE: 2001-07-19  
;; NUMBER OF SEQ ID NOS: 90  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 26  
;; LENGTH: 594  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-199-869-26

Query Match 46.5%; Score 594; DB 15; Length 594;  
Best Local Similarity 100.0%; Pred. No. 2.le-305;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 634 ATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTGAGTTTCATTTGTC 693  
Db 1 ATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTGAGTTTCATTTGTC 60  
  
QY 694 TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACAATGATTGATTACTGGCAATC 753  
Db 61 TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACAATGATTGATTACTGGCAATC 120  
  
QY 754 ACGCGTATTACATCTCTGTGTGATGACAGTGTTCAGGCGGAACTCTCAACTCCAG 813  
Db 121 ACGCGTATTACATCTCTGTGTGATGACAGTGTTCAGGCGGAACTCTCAACTCCAG 180  
  
QY 814 AGGCTGGAGTCACTTGAAGGTACTTAGAATGATGAGATTTTGGGTGATTAAAGCTT 873  
Db 181 AGGCTGGAGTCACTTGAAGGTACTTAGAATGATGAGATTTTGGGTGATTAAAGCTT 240  
  
QY 874 GCCGTGCTATCTTGTGTTTTCAGACACTCGGTTGACTCTCAACGTTGCTACCGAG 933  
Db 241 GCCGTGCTATCTTGTGTTTTCAGACACTCGGTTGACTCTCAACGTTGCTACCGAG 300  
  
QY 934 ATGGTTATGTTACTTGTCTTCACTTGTGTGCCATGGCAATCTTTAGTGCATTTCTCAG 993  
Db 301 ATGGTTATGTTACTTGTCTTCACTTGTGTGCCATGGCAATCTTTAGTGCATTTCTCAG 360  
  
QY 994 CTTCTTGAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTTACAGCAATTCCTGCT 1053  
Db 361 CTTCTTGAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTTACAGCAATTCCTGCT 420  
  
QY 1054 GCCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGGAGATATGATCTATC 1113  
Db 421 GCCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGGAGATATGATCTATC 480  
  
QY 1114 ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTGTGTCAGTGGAAATGTTCTATTGCA 1173  
Db 481 ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTGTGTCAGTGGAAATGTTCTATTGCA 540  
  
QY 1174 TTACCTATCACTTTTATCTACATAGCTTTTGGCAGTGTATCATGAGCTCAAG 1227  
Db 541 TTACCTATCACTTTTATCTACATAGCTTTTGGCAGTGTATCATGAGCTCAAG 594

RESULT 7  
US-10-199-869-27  
;; Sequence 27, Application US/10199869  
;; Publication No. US20030152953A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bristol-Myers Squibb Company  
;; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
;; FILE REFERENCE: K-alpha2  
US-10-199-869-27

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; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2/
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-27

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Query Match	31.3%	Score 400	DB 15	Length 417
Best Local Similarity	100.0%	Pred. No. 4.2e-202		
Matches 400	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	31	GTGGTCTGAACGTGGCGGGCCCGGTATTCGCTCCGGGAGACTCTGAAGACTTC	90	
DB	1	GTGGTCTGAACGTGGCGGGCCCGGTATTCGCTCTCCGGGAGCTGCTGAAGACTTC	60	
QY	91	CGCGTGGCCCGCGTGAGCCGGCTGACGGTGCAGCGTCCGCTCGAGCGGAGAGTGCTCGAGGTG	150	
DB	61	CGCGTGGCCCGCGTGAGCCGGCTGACGGTGCAGCGTCCGCTCGAGCGCGAGTGCTCGAGGTG	120	
QY	151	TCCGACGACTACGACCGGAGCGGACAGAGTACTTCTTCGACGGGACTCGGAGGCTTC	210	
DB	121	TGCAGCAGTACGACCGGAGCGGACAGAGTACTTCTTCGACCGGACTTCGGAGGCGCTTC	180	
QY	211	GGCTTCATCTGCTCTACGTGCGGGCCACGGCAAGCTCGCTTCGCGCGCGGATGTGC	270	
DB	181	GGCTTCATCTGCTCTACGTGCGGGCCACGGCAAGCTGCGCTTCGCGCGCGGATGTGC	240	
QY	271	GAGCTCTCCTTCTTAAACAGAGATGATCTACTGGGGCTGGAGGGCGCGCACTCGAGTAC	330	
DB	241	GAGCTCTCCTTCTTAAACAGAGATGATCTACTGGGGCTGGAGGGCGCGCACTCGAGTAC	300	
QY	331	TGCTTGCCAGCGCGCTTCGACGACCGATGTCCGACACCTACACCTTCTACTTCGGCCGAC	390	
DB	301	TGCTTGCCAGCGCGCTTCGACGACCGATGTCCGACACCTACACCTTCTACTTCGGCCGAC	360	
QY	391	GAGCGGGCGTGTGGGCCCGGACGAGGGCGCGCCCGGCG	430	
DB	361	GAGCGGGCGTGTGGGCCCGGACGAGGGCGCGCCCGGCG	400	

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RESULT 8
US-09-852-386-25
/ Sequence 25, Application US/09852386
/ Publication No. US20030064433A1
/ GENERAL INFORMATION:
/
/ APPLICANT: Roberts, Steven L.
/ APPLICANT: Benjamin, Christopher
/ APPLICANT: Karnovsky, Alla M.
/ APPLICANT: Ruble, Cara L.
/
/ TITLE OF INVENTION: Human Ion Channels
/
/ FILE REFERENCE: 00133.US1
/
/ CURRENT APPLICATION NUMBER: US/09/852,386
/ CURRENT FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 60/203,305
/ PRIOR FILING DATE: 2000-05-10
/ PRIOR APPLICATION NUMBER: 60/207,092
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/206,526
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,033
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/207,093
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/216,893
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 60/237,873
/ PRIOR FILING DATE: 2000-10-04

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1  PRIOR APPLICATION NUMBER: 60/223,243
2  PRIOR FILING DATE: 2000-08-04
3  NUMBER OF SEQ ID NOS: 88
4  SOFTWARE: PatentIn version 3.0
5  SEQ ID NO 25
6  LENGTH: 461
7  TYPE: DNA
8  ORGANISM: Homo sapiens
9  US-09-852-386-25

```

Query Match	27.2%;	Score 347;	DB 13;	Length 461;
Best Local Similarity	100.0%;	Pred. No. 7e-174;		
Matches 347;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	932	AGATGGTTATGTTACTTGTCCTTCATTTGTTGCCATGGCAATCTTTAGTGCACCTTCTC	991	
Db	49	AGATGGTTATGTTACTTGTCCTTCATTTGTTGCCATGGCAATCTTTAGTGCACCTTCTC	108	
QY	992	AGCTTCTTGAAACATGGCTGGACCTGGAACAATCCAAACAGGACTTTTACCAGCATTTCCCTG	1051	
Db	109	AGCTTCTTGAAACATGGCTGGACCTGGAACAATCCAAACAGGACTTTTACCAGCATTTCCCTG	168	
QY	1052	CTCCCTGCTGGTGGGTGATTTATCTCTATGACTACAGTTGGCTATGGAGATATGATACCTTA	1111	
Db	169	CTCCCTGCTGGTGGGTGATTTATCTCTATGACTACAGTTGGCTATGGAGATATGATACCTTA	228	
QY	1112	TCACAGTGGCTGGAAGAAATCTTGGAGGAGTTTGTTGTTCACGTGGAATGTTCTATTGG	1171	
Db	229	TCACAGTGGCTGGAAGAAATCTTGGAGGAGTTTGTTGTTCACGTGGAATGTTCTATTGG	288	
QY	1172	CATTACTATCATCTTTTATCTACCATAGCTTTCTGCAGTGGTTATCATGAGCTCAAGTTTA	1231	
Db	289	CATTACTATCATCTTTTATCTACCATAGCTTTCTGCAGTGGTTATCATGAGCTCAAGTTTA	348	
QY	1232	GATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAAATTCCTGAAATTA	1278	
Db	349	GATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAAATTCCTGAAATTA	395	

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RESULT 9
US-09-989-920-7/c
; Sequence 7, Application US/09899920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-7

Query Match 25.9%; Score 331; DB 9; Length 777;
Best Local Similarity 100.0%; Pred.No. 2.3e-165;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 948 TGCTTCATTGTGTGTCATGGCAATCTTTAGTGCACCTTTCTCAGCTTCTTGAAATGG 1007
DB 662 TGCTTCATTGTGTGTCATGGCAATCTTTAGTGCACCTTTCTCAGCTTCTTGAAATGG 603
QY 1008 GCTGACCTGGAAACATCCAAACAGGACTTTACAGCATTTCTGCTGCTCTGCTGGGT 1067

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Db	602	GCTGGACCTTGGAAACATCCAAACAGGACTTTTACGAGCATTCCTGCTGCTCTGGTGGGT	543
Qy	1068	GATTATCTCTATGACTACTACAGTTGGCTATGGAGATATGTATCCTATCACAGTGCCTCGGAAG	1127
Db	542	GATTATCTCTATGACTACAGTTGGCTATGGAGATATGTATCCTATCACAGTGCCTCGGAAG	483
Qy	1128	AATTCTTGGAGGACTTTGTGTTGTTCAGTGGAAATGTTCCTATTGGCAATTACCTATCACATTT	1187
Db	482	AATTCTTGGAGGAGTTTGTGTTGTTCAGTGGAAATGTTCCTATTGGCAATTACCTATCACATTT	423
Qy	1188	TATCTACCATAGCTTTGTGCACTGTTTATCATGAGCTCAAGTTTATAGATCTGCTAGGTATAG	1247
Db	422	TATCTACCATAGCTTTGTGCACTGTTTATCATGAGCTCAAGTTTATAGATCTGCTAGGTATAG	363
Qy	1248	TAGAGGCTCTCCACTGAATTCCTGAATTA	1278
Db	362	TAGAGGCTCTCCACTGAATTCCTGAATTA	332

RESULT 10  
 US-09-989-920-8  
 ; Sequence 8, Application US/09989920  
 ; Patent NO. US20020172957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Macina, Roberto  
 ; APPLICANT: Recipon, Hervé  
 ; APPLICANT: Chen, Sei-Yu  
 ; APPLICANT: Sun, Yongming  
 ; APPLICANT: Liu, Chenghua  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Products  
 ; FILE REFERENCE: DX-0291  
 ; CURRENT APPLICATION NUMBER: US/09/989,920  
 ; CURRENT FILING DATE: 2001-11-21  
 ; PRIOR APPLICATION NUMBER: 60/252,500  
 ; PRIOR FILING DATE: 2000-11-22  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 911  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-09-989-920-8

Query Match	17.0%;	Score 217;	DB 9;	Length 911;
Best Local Similarity	100.0%;	Prod. No. 1.1e-104;		
Matches 217;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
QY	1062	GTGGGTGATTCTCTATGACTACAGTTGGCTATGGAGATATGATCTCTATCACAGTGCC	1121	
Db	229	GTGGGTGATTCTCTATGACTACAGTTGGCTATGGAGATATGATCTCTATCACAGTGCC	288	
QY	1122	TGGAAGAANTCTTGAGAGAGTTGTGTTCAGTGGAAATGTGTTCTATTGGCATTACCTAT	1181	
Db	289	TGGAAGAANTCTTGAGAGAGTTGTGTGTTCAGTGGAAATGTGTTCTATTGGCATTACCTAT	348	
QY	1182	CACITTTTATCTACCATAGCTTTGTCAGTGTATTATCATGAGCTCAAGTTTATGATCTGCTAG	1241	
Db	349	CACITTTTATCTACCATAGCTTTGTCAGTGTATTATCATGAGCTCAAGTTTATGATCTGCTAG	408	
QY	1242	GTATAGTAGGCGCTCTCCACTGAATTCCCTGAATTAA	1278	
Db	409	GTATAGTAGGCGCTCTCCACTGAATTCCCTGAATTAA	445	

RESULT 11  
US-10-199-869-28  
; Sequence 28, Application US/10199869  
; Publication No. US20030152953A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
; TITLE OF INVENTION: K+alphaM2  
; FILE REFERENCE: D0161 NP

```

; CURRENT APPLICATION NUMBER: US/10/199,869.
;
; CURRENT FILING DATE: 2002-07-19
;
; PRIOR APPLICATION NUMBER: US 60/306,577
;
; PRIOR FILING DATE: 2001-07-19
;
; NUMBER OF SEQ ID NOS: 90
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 28
;
; LENGTH: 138
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; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-10-199-869-28

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	Query Match	10.8%	Score 138	DB 15	Length 138
	Best Local Similarity	100.0%	Pred. No. 1.4e-62		
	Matches 138	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	454	CGCTGGCTGAGCGCATGCGCGGACCTTCGAGGAGCCACGTCGTCGCTGGCCGCGCAG	513		
Db	1	CGCTGGCTGAGCGCATGCGCGGACCTTCGAGGAGCCACGTCGTCGCTGGCCGCGCAG	60		
Qy	514	ATCCTGCTAGCGTGCCTGGTTCGTCATCGTCATGCTGGTGCCTGTGCGCCAGC	573		
Db	61	ATCCTGCTAGCGTGCCTGGTTCGTCATCGTCATGCTGGTGCCTGTGCGCCAGC	120		
Qy	574	ACGTTGCCCGACTGGCGC	591		
Db	121	ACGTTGCCCGACTGGCGC	138		

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RESULT 12
US-10-199-869-30/c
; Sequence 30, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUBU
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUBU
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 80
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-199-869-30

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	Query Match	6.3%	Score 80;	DB 15;	Length 80;
	Best Local Similarity	100.0%	Pred. No. 1.1e-31;		
	Matches 80;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	751	ATCAGCGCGTATTACATCTCTGTGTGTGATGACAGTGTGTTTACAGGGCAGAACTCTCAACTC	810		
DB	80	ATCAGCGCGTATTACATCTCTGTGTGATGACAGTGTGTTTACAGGGCAGAACTCTCAACTC	21		
QY	811	CAGAGGGCTGGAGTCACCTT	830		
DB	20	CAGAGGGCTGGAGTCACCTT	1		

RESULT 13  
US-10-199-869-89/c  
; Sequence 89, Application US/10199869  
; Publication NO. US20030152953A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING  
; TITLE OF INVENTION: K-alphaM2  
; FILE REFERENCE: D0161 NP  
; CURRENT APPLICATION NUMBER: US/10/199,869

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; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 89
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-89

Query Match          2.3%; Score 30; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 931 GAGATGGTTATGTTACTTGTCTTCATTGT 960
    |||||
Db 30 GAGATGGTTATGTTACTTGTCTTCATTGT 1

RESULT 14
US-10-114-270-268
; Sequence 268, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kexuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Zhaozhong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liette, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stoner, David J.
; APPLICANT: Macdougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10

; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 89
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-89

Query Match          2.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 865 ATTAGCTTGCCTCACTTCATTGG 890
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Db 1 ATTAGCTTGCCTCACTTCATTGG 26

RESULT 15
US-10-199-869-38/c
; Sequence 38, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 38
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-38

Query Match          2.0%; Score 25; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1251 GAGCTCTCCACTGAATTCCTGAAT 1275
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Db 37 GAGCTCTCCACTGAATTCCTGAAT 13

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:32:13 ; Search time 5116 Seconds  
(without alignments)  
10827.286 Million cell updates/sec

Title: US-10-016-647-1  
Perfect score: 1278  
Sequence: 1 atgaccttcggcgagcggg.....ccactgaattcctgaattaa 1278

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_mus.\*
- 33: em\_htg\_other.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rtd.\*
- 36: em\_htg\_nam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1278	100.0	1278	6	AX511260	AX511260 Sequence
2	1278	100.0	1844	6	AX511262	AX511262 Sequence
3	1278	100.0	3670	9	AF454547	AF454547 Homo sapi
4	840	65.7	2312	6	AX392945	AX392945 Sequence
5	729	57.0	2235	6	AX478109	AX478109 Sequence
6	649	50.8	151367	9	AC025750	AC025750 Homo sapi
7	647	50.6	1311	9	AB070604	AB070604 Homo sapi
8	647	50.6	1947	6	AX641934	AX641934 Sequence
9	647	50.6	1947	9	AF348982	AF348982 Homo sapi
10	647	50.6	3703	9	AF454548	AF454548 Homo sapi
11	347	27.2	461	6	AX319980	AX319980 Sequence
12	331	25.9	777	6	AX534980	AX534980 Sequence
13	217	17.0	911	6	AX534981	AX534981 Sequence
14	80	6.3	1302	9	AF450110	AF450110 Homo sapi
15	80	6.3	1744	10	AF454549	AF454549 Rattus no
16	80	6.3	1777	10	AF454550	AF454550 Rattus no
17	80	6.3	219807	2	AC098764	AC098764 Rattus no
18	80	6.3	259704	2	AC112092	AC112092 Rattus no
19	80	6.3	288099	2	AC133407	AC133407 Rattus no
20	78	6.1	702	9	HS325071	AJ325071 Homo sapi
21	71	5.6	3323	10	AF454551	AF454551 Mus muscu
22	71	5.6	3356	10	AF454552	AF454552 Mus muscu
23	71	5.6	5775	6	AX641960	AX641960 Sequence
24	71	5.6	68831	2	AC101224	AC101224 Mus muscu
25	71	5.5	209523	10	AC084386	AC084386 Mus muscu
26	70	5.5	1038	10	AB070605	AB070605 Rattus no

ALIGNMENTS

RESULT 1  
LOCUS AX511260 1278 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 1 from Patent WO0250271.  
ACCESSION AX511260  
VERSION AX511260.1 GI:233921138  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Fiddle, C.J., Hilbun, E. and Turner, C.A.  
TITLE Novel human ion channel protein and polynucleotides encoding the  
JOURNAL Same  
Patent: WO 0250271-A 1 27-JUN-2002;  
Lexicon Genetics Incorporated (US)  
FEATURES  
source  
1..1278  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1278; DB 6; Length 1278;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGACCTTCGGCGCAGCGGGCGGCTCGTGTGCTGACCTGGCGGCGCGCGGTAT 60  
Db 1 ATGACCTTCGGCGCAGCGGGCGGCTCGTGTGCTGACCTGGCGGCGCGCGGTAT 60  
Qy 61 TCGCTGTCCCGGGAGCTGCTGAAGCACTTCCCGTGGCGCGCGGTGACCGCGCTCACGGC 120

Pred. No. is the number of results predicted by chance to have a

Db 61 TCGCTGTCGGGAGCTGTGAAGACTTCCCGTGGCCGCTGAGCCGGCTGCACGGC 120  
Qy 121 TCGCGCTCCGAGCGCGACGTGCTCGAGGTGTGCGACGACTACGACCGCGAGCCCAACGAG 180  
Db 121 TCGCGCTCCGAGCGCGACGTGCTCGAGGTGTGCGACGACTACGACCGCGAGCCCAACGAG 180  
Qy 181 TACTTCTTCACCGCGACTCGAGCGCTTCGGCTTCATCTGCTCTACGTCGCGCGCCAC 240  
Db 181 TACTTCTTCACCGCGACTCGAGCGCTTCGGCTTCATCTGCTCTACGTCGCGCGCCAC 240  
Qy 241 GCGAAGCTGGCTTCGCGCCGCGAGATGCGAGCTTCCTTCTACAAAGAGATGATCTAC 300  
Db 241 GCGAAGCTGGCTTCGCGCCGCGAGATGCGAGCTTCCTTCTACAAAGAGATGATCTAC 300  
Qy 301 TGGGGCTTGAGGCGCGACCTCGAGTACTGTGCCAGCGCGCTTCGACGACCGCATG 360  
Db 301 TGGGGCTTGAGGCGCGACCTCGAGTACTGTGCCAGCGCGCTTCGACGACCGCATG 360  
Qy 361 TCCGACACCTACACCTTCTACTCGCGCGACGAGCGCGCTGTGGCGCGCGACGAGCGC 420  
Db 361 TCCGACACCTACACCTTCTACTCGCGCGACGAGCGCGCTGTGGCGCGCGACGAGCGC 420  
Qy 421 CGCCCGCGCGCGCGAGCGCTCCCTCCAGGGCTGGCTGAGCGCATGCGCGCGAC 480  
Db 421 CGCCCGCGCGCGCGAGCGCTCCCTCCAGGGCTGGCTGAGCGCATGCGCGCGAC 480  
Qy 481 TTCGAGGAGCCACGTGCTGGCGCGCGACGATCTGCTAGCGTGTGGTGTGTTTC 540  
Db 481 TTCGAGGAGCCACGTGCTGGCGCGCGACGATCTGCTAGCGTGTGGTGTGTTTC 540  
Qy 541 GTGATCGTGTCCATGTGTGTGGCGCGACGAGTGTGCCCGACGTGGCGCGACGAGCGC 600  
Db 541 GTGATCGTGTCCATGTGTGTGGCGCGACGAGTGTGCCCGACGTGGCGCGACGAGCGC 600  
Qy 601 GCGGACAAACGCGAGCTGGATGACCGGAGCGAGATTAATTGAGCTATCTGCATAGTTGG 660  
Db 601 GCGGACAAACGCGAGCTGGATGACCGGAGCGAGATTAATTGAGCTATCTGCATAGTTGG 660  
Qy 661 TTCACTCCGAGTGCATGTGAGGTTCAATGTTCTCCAAAACAAAGTGTGAGTTGTCAAG 720  
Db 661 TTCACTCCGAGTGCATGTGAGGTTCAATGTTCTCCAAAACAAAGTGTGAGTTGTCAAG 720  
Qy 721 AGACCCCTGAGCATATGATTTACTGGCAATCAGCCGCTATTACATCTCTGTTGTGATG 780  
Db 721 AGACCCCTGAGCATATGATTTACTGGCAATCAGCCGCTATTACATCTCTGTTGTGATG 780  
Qy 781 ACAGTGTTTACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTTGAGGGTACTT 840  
Db 781 ACAGTGTTTACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTTGAGGGTACTT 840  
Qy 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCGGTCACTTCAATGGTCTTCAGACA 900  
Db 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCGGTCACTTCAATGGTCTTCAGACA 900  
Qy 901 CTGGTTTGTACTCTCAACCGTGTCTACCGAGAGATGTTATGTTACTTGTCTTCAATTTGT 960  
Db 901 CTGGTTTGTACTCTCAACCGTGTCTACCGAGAGATGTTATGTTACTTGTCTTCAATTTGT 960  
Qy 961 GTTGCCATGGCAATCTTTAGTGCATTTCTCAGCTTCTTGAAATGGGTGGACCTGGAA 1020  
Db 961 GTTGCCATGGCAATCTTTAGTGCATTTCTCAGCTTCTTGAAATGGGTGGACCTGGAA 1020  
Qy 1021 ACATCCAAAGGACTTTACAGCATTCCTGCTGCTGCTGGTGGTGAATATCTCTATG 1080  
Db 1021 ACATCCAAAGGACTTTACAGCATTCCTGCTGCTGCTGGTGGTGAATATCTCTATG 1080  
Qy 1081 ACTACAGTTGGCTATGAGATATGATTCCTATCAGATGCTGGAAAGATTTCTTGAGGA 1140  
Db 1081 ACTACAGTTGGCTATGAGATATGATTCCTATCAGATGCTGGAAAGATTTCTTGAGGA 1140  
Qy 1141 GTTGTGTTGTCAGTGGAAATTTCTATTGGCATTTACCTATCACTTTTATACCATAGC 1200  
Db 1141 GTTGTGTTGTCAGTGGAAATTTCTATTGGCATTTACCTATCACTTTTATACCATAGC 1200

Qy 1201 TTTGTGCACTGTATCATGTAGCTCAAGTTAGATCTGCTAGGTATAGTAGAGCCTCTCC 1260  
Db 1201 TTTGTGCACTGTATCATGTAGCTCAAGTTAGATCTGCTAGGTATAGTAGAGCCTCTCC 1260  
Qy 1261 ACTGAATTCCTCAATTA 1278  
Db 1261 ACTGAATTCCTCAATTA 1278  
RESULT 2  
AX511262 1844 bp DNA linear PAT 27-SEP-2002  
LOCUS Sequence 3 from Patent WO0250271.  
DEFINITION AX511262  
ACCESSION AX511262  
VERSION AX511262.1 GI:23392139  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Priddle, C.J., Hilbun, E. and Turner, C.A.  
TITLE Novel human ion channel protein and polynucleotides encoding the same  
JOURNAL Patent: WO 0250271-A 3 27-JUN-2002;  
Lexicon Genetics Incorporated (US)  
FEATURES  
source 1. 1844  
/organism="Homo sapiens"  
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ORIGIN  
Query Match 100.0%; Score 1278; DB 6; Length 1844;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGACCTTCGGGCGAGCGGGCGGCTCGTGTGTGTGCTGAACGTGGCGGGCGCGGTAT 60  
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Qy 121 TCCCGCTCCGAGCGAGCGTGTCTCAGGTTGTGCGAGCTACGACCGCGAGCGCAACGAG 180  
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Qy 181 TACTTCTTCGACCGCGACTCGGAGCGCTTCGGCTTCATCTGCTACGTGCGCGGCAC 240  
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Qy 241 GCGAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACAAAGAGATGATCTAC 300  
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Qy 361 TCCGACACCTACACCTTCTACTCGCGCGAGAGCGCGCGCTGTGGCGCGCGAGCGCG 420  
Db 817 TCCGACACCTACACCTTCTACTCGCGCGAGAGCGCGCGCTGTGGCGCGCGAGCGCG 876  
Qy 421 CGCCCGCGCGCGCGAGCGCGCTTCCTCCAGGGCTGGCTGAGCGCATGCGCGCGAC 480  
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Db 937 TTCGAGGAGCCACGTGCTGCTGGCGCGCGAGATCCTGGCTAGCGTGTGGTGTGTTTC 996





ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Tang, Y.T., Yue, H., Nguyen, D.B., Hafalia, A.J., Elliott, V.S., Lu, Y.,  
Walia, N.K., Yao, M.G., Raughn, M.R., Gandhi, A.R., Ding, L.,  
Sanjanwala, M., Ramkumar, J., Arvizu, C., Gietzen, K.J., Lai, P.G.,  
Azimzai, Y., Khan, F.A., Thangavelu, K., Thornton, M., Lu, D.A.,  
Tribouley, C.M., Warren, B.A., Ison, C.H., Das, D., Raumann, B.E.,  
Policky, J.L. and Kearney, L.  
TITLE Transposers and ion channels  
JOURNAL Patent: WO 0240541-A 39 23-MAY-2002;  
Incyte Genomics, Inc. (US)  
FEATURES  
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/note="Incyte ID No: 7482060CB1"

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Query Match 57.0%; Score 729; DB 6; Length 2235;  
Best Local Similarity 100.0%; Pred. 0;  
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 514 ATCCCTGGCTAGCGTCTCGGTGGTGTTCGTGATCGTCCATGGTGGTCTGTGGCCAGC 573  
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Db 980 AGTTGCCCGACTGCGCAACGACCCCGCAACACCGACCGCTGGATGACCGGAGCAGG 1039  
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QY 1234 TCTGCTAGG 1242  
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RESULT 6  
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DEFINITION Homo sapiens BAC clone RP11-804P20 from 2, complete sequence.  
ACCESSION AC025750  
VERSION AC025750.10 GI:18098549  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 151367)  
AUTHORS Sulston, J.E. and Waterston, R.  
TITLE Toward a complete human genome sequence  
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
MEDLINE 93063792  
PUBMED 9847074  
REFERENCE 2 (bases 1 to 151367)  
AUTHORS Tomlinson, C., Cotton, M. and Doeber, A.  
TITLE The sequence of Homo sapiens BAC clone RP11-804P20  
JOURNAL Unpublished (2002)  
REFERENCE 3 (bases 1 to 151367)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (13-MAR-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 4 (bases 1 to 151367)  
AUTHORS Waterston, R.  
TITLE Direct Submission  
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Jan 9, 2002 this sequence version replaced gi:13431263.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [sapiens@wustl.edu](mailto:sapiens@wustl.edu)  
----- Summary Statistics  
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Center project name: H\_NH0804P20

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RP11 human BAC library was made from the blood of one male donor, as described by Osagawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Cateneese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong



and coworkers at the Roswell Park Cancer Institute  
(http://baopac.med.buffalo.edu)

VECTOR: pBACE3.6

# NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-299C5, 2000 bp overlap; the clone sequenced to the right is RP11-729W8. Actual start of this clone is at base position 157736 of RP11-299C5; actual end is at base position 151367 of RP11-804P20.

Data from AC074375 and AC006038 was used to finish this clone, AC025750. Polymorphisms have been identified between AC025750 and AC074375. The sequence from 40567 to 41115, from 40991 to 41115 are covered only by PCR products from clone DNA. There is an unresolved homopolymeric run between 39229 and 39243. There is an unresolved region between 13476 and 132479.

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4999. .5301

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Best Local Similarity 100.0%; Pred. No. 0;

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QY 690 TGCTCCAAAACAAGTGTCAGTTTGTCAAGAGACCCCTCAACATCATTTGATTTACTGGC 749

Db 8422 TGCTCCAAAACAAGTGTCAGTTTGTCAAGAGACCCCTCAACATCATTTGATTTACTGGC 8363

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DEFINITION  
AB070604 1311 bp mRNA linear PRI 23-MAR-2002  
cds.  
AB070604  
VERSION  
AB070604.1 GI:19916472  
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Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 Sano, Y., Mochizuki, S., Miyake, A., Kitada, C., Inamura, K., Yokoi, H.,  
Nozawa, K., Matsushima, H. and Furuichi, K.  
TITLE  
Molecular cloning and characterization of Kv6.3, a novel modulatory  
subunit for voltage-gated K+ channel Kv2.1  
JOURNAL  
FEBS Lett. 513, 230-234 (2002)  
REFERENCE  
2 (bases 1 to 1311)  
AUTHORS  
Sano, Y. and Mochizuki, S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (24-AUG-2001) Yorikata Sano, Yamanouchi Pharmaceutical  
Co., Ltd, Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba,  
Ibaraki 305-8585, Japan (E-mail: sano.yorikata@yamanouchi.co.jp,  
Tel: 81-298-52-5111, Fax: 81-298-52-2965).

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ORIGIN  
Query Match 50.6%; Score 647; DB 9; Length 1311;  
Best Local Similarity 100.0%; Pred. No. 0;  
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DB 1145 TCACAGTGGCTGGAAGAAATTTCTGGAGGAGTTTGTGTGTGCTAGTGGAAATTTCTATTGG 1204  
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DB 1205 CATTAACATATCACTTTTATCATATAGCTTTTGTGAGTGTTCATGAGCTCAAGTTTA 1264  
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DB 1265 GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1311

RESULT 8  
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LOCUS  
DEFINITION  
AX641934 Sequence 3 from Patent WO02096944.  
ACCESSION  
AX641934.1 GI:28474564  
VERSION  
AX641934.1  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1	Snyders,D.J., Ottschytch,N., Raes,A. and van Hoorick,D. New heterotetrameric potassium channels and uses thereof Patent: WO 0209644-A 3 05-DEC-2002; Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
AUTHORS		
TITLE		
JOURNAL		
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QY	632	GGATAATTGAAGCTATCTGCATAGTGTGGTTCACTGCCAGTGCATCGTAGGTTCAATG 691
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LOCUS		
DEFINITION		Homo sapiens voltage-gated potassium channel Kv10.1 mRNA, complete cds.
ACCESSION		AF348982
VERSION		AF348982.1 GI:19070536
KEYWORDS		
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		1 (bases 1 to 1947) Ottschytch,N., Raes,A., Van Hoorick,D. and Snyders,D.J. Obligatory heterotetramerization of three previously uncharacterized Kv channel alpha -subunits identified in the human genome Proc. Natl. Acad. Sci. U.S.A. 99 (12), 7986-7991 (2002)
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (12), 7986-7991 (2002)
MEDLINE		22056098
PMID		12060745
REFERENCE		2 (bases 1 to 1947) Ottschytch,N., van Hoorick,D., Raes,A.L. and Snyders,D.J. Direct Submission Submitted (14-FEB-2001) Molecular Biophysics, VIB (Flanders Inst. Biotechnology & University of Antwerp, Universiteitsplein 1, Antwerp 2610, Belgium Location/Qualifiers 1. .1947 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="2" /map="2p21" /map="2p21" 596..1906 /codon_start=1 /product="voltage-gated potassium channel Kv10.1" /protein_id="AAL83909.1" /db_xref="GI:19070537"
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QY	1052	CTGCCGTGCTGGTGGTGAATTTCTCTATGACTACAGTTGGCTATGGAGATATGATCTTA 1111
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QY	1172	CATTACTATCACTTTTATCTACCATAGCTTTGTGAGTGTGTTATCATGAGCTCAAGTTTA 1231
Db	1800	CATTACTATCACTTTTATCTACCATAGCTTTGTGAGTGTGTTATCATGAGCTCAAGTTTA 1859
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Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
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LOCUS
DEFINITION Sequence 7 from Patent WO02068633.
ACCESSION AX534980
VERSION AX534980.1 GI:25261559
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 7 06-SEP-2002;
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QY 1008 GCTGACCTGGAAACATCCCAAGACCTTTACAGACCTTTCTGCTGCTCTGCTGGGT 1067
DB 602 GCTGACCTGGAAACATCCCAAGACCTTTACAGACCTTTCTGCTGCTCTGCTGGGT 543

QY 1068 GATTATCTATGATACATGTTGGTATGGAGATATGATCTATCATGAGTGGCTGGAAG 1127
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AX534981
LOCUS
DEFINITION Sequence 8 from Patent WO02068633.
ACCESSION AX534981
VERSION AX534981.1 GI:25261562
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 8 06-SEP-2002;
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LOCUS
DEFINITION Homo sapiens voltage-gated potassium channel subunit Kv6.4 mRNA, complete cds.
ACCESSION AF450110
VERSION AF450110.1 GI:31295623
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Preising-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.
TITLE Cloning and characterization of two novel gamma Kv subunits
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1302)
AUTHORS Preising-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.
TITLE Direct Submission

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JOURNAL Submitted (23-NOV-2001) University of Marburg, Institute of Physiology, Deutschshausstrasse 1-2, Marburg 35037, Germany

FEATURES Location/Qualifiers

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Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 470 AAGCTCGCTTCGCGCGCGGATGTCGAGCTCTCTTCTACACGAGATGATCTACTGG 529

QY 304 GGCCTGGAGGGCGGCACCT 323

DB 530 GGCCTGGAGGGCGGCACCT 549

Search completed: April 19, 2004, 18:31:42

Job time : 5126 secs

JOURNAL Submitted (23-NOV-2001) University of Marburg, Institute of Physiology, Deutschshausstrasse 1-2, Marburg 35037, Germany

FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 5.8e-30;

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DB 304 GGCCTGGAGGGCGGCACCT 323

RESULT 15

AF454549

LOCUS Rattus norvegicus voltage-gated potassium channel subunit Kv10.1a

DEFINITION mRNA, complete cds, alternatively spliced.

ACCESSION AF454549

VERSION AF454549.1 GI:22164085

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 1744)

AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.

TITLE Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1744)

AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.

TITLE Direct Submission

JOURNAL Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA

FEATURES Location/Qualifiers

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GenCore version 5.1.6  
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Word size : 24

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	729	57.0	2235	6	ABK83228	Abk83228 Human tra
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ALIGNMENTS

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ID ABN83930 standard; cDNA; 1278 BP.  
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AC ABN83930;  
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DT 06-SEP-2002 (first entry)  
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DE Human voltage-gated potassium channel-like protein encoding cDNA.  
XX  
XX Human; voltage-gated potassium channel; ion channel; neuroprotective;  
KW therapeutic; diagnostic; pharmacogenic; gene therapy; SNP;  
KW single nucleotide polymorphism; foetal brain; brain; cerebellum;  
KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;  
KW foetal liver; liver; testis; thyroid; salivary gland; stomach;  
KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;  
KW 12 week old embryo; adenocarcinoma; osteosarcoma; Gene; ss.  
OS Homo sapiens.  
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XX 27-JUN-2002.  
XX  
XX 10-DEC-2001; 2001WO-US048050.  
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XX 20-DEC-2000; 2000US-0257932P.  
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XX (LEXI-) LEXICON GENETICS INC.  
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XX Fiddle CJ, Hilbun E, Turner CA;  
XX  
XX WPI; 2002-508799/54.  
DR P-PSDB; ABB83073.  
DR  
XX Human ion channel polynucleotide useful in therapeutic, diagnostic and  
PT pharmacogenomic applications.  
XX  
XX Claim 1; Page 34; 36pp; English.  
XX  
CC The invention relates to a novel human ion channel polynucleotide that  
CC shares structural similarity with voltage-gated potassium channel  
CC proteins. The activity of the protein of the invention may be described  
CC as neuroprotective. The protein of the invention is useful in  
CC therapeutic, diagnostic and pharmacogenomic applications, for example to  
CC identify mutations associated with a particular disease, as a diagnostic  
CC or prognostic assay, or in gene therapy. The protein of the invention has  
CC been found to be expressed in human foetal brain, brain, cerebellum,  
CC pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal  
CC heart, liver, testis, thyroid, salivary gland, stomach, skeletal muscle,  
CC adenocarcinoma and osteosarcoma cells. The current sequence represents  
CC the human voltage-gated potassium channel-like protein encoding cDNA  
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Best Local Similarity 100.0%; Pred. No. 0;  
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 961 GTTGCCATGCGATCTTTAGTGCATTTCTAGCTTCTTGAACATGGGCTGAGCTGGA 1020  
 1021 ACATCAACAGGACTTTTACGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 1021 ACATCAACAGGACTTTTACGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 1081 ACTACAGTGTGCTATGAGATATGATTCCTATCAGAGTCCCTGGAAGATTTCTGAGA 1140  
 1081 ACTACAGTGTGCTATGAGATATGATTCCTATCAGAGTCCCTGGAAGATTTCTGAGA 1140  
 1141 GTTGTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200

Db 1141 GTTGTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
 Qy 1201 TTTGTGAGGTGTTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1260  
 Db 1201 TTTGTGAGGTGTTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1260  
 Qy 1261 ACTGAATTCCTGAATTAA 1278  
 Db 1261 ACTGAATTCCTGAATTAA 1278

RESULT 2  
 AEN83931  
 ID AEN83931 standard; DNA; 1844 BP.  
 AC AEN83931;  
 XX  
 DT 06-SEP-2002 (first entry)  
 XX Human voltage-gated potassium channel-like protein encoding sequence.  
 DE Human; voltage-gated potassium channel; ion channel; neuroprotective;  
 KW therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;  
 KW single nucleotide polymorphism; foetal brain; brain; cerebellum;  
 KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;  
 KW foetal liver; liver; testis; thyroid; salivary gland; stomach;  
 KW skeletal muscle; heart; uterus; adipose; hypophalamus; ovary; aorta;  
 KW 12 week old embryo; adenocarcinoma; osteosarcoma; Gene; ds.  
 XX Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT 5'UTR 1..456  
 FT CDS /\*tag= a  
 457..1734  
 FT /\*tag= b  
 /\*product= "voltage-gated potassium channel-like protein"  
 FT variation replace(888,C)  
 /\*tag= c  
 /\*standard\_name= "single nucleotide polymorphism"  
 FT 3'UTR 1735..1844  
 /\*tag= d  
 XX WO200250271-A2.  
 XX  
 XX 27-JUN-2002.  
 XX  
 PF 10-DEC-2001; 2001WO-US048050.  
 XX  
 PR 20-DEC-2000; 2000US-0257932P.  
 XX  
 XX (LEXI-) LEXICON GENETICS INC.  
 PA Friddle CJ, Hilbun E, Turner CA;  
 XX  
 XX WPI; 2002-508799/54.  
 DR P-PSDB; ABB83073.  
 XX  
 PT Human ion channel polynucleotide useful in therapeutic, diagnostic and  
 PT pharmacogenomic applications.  
 XX  
 PS Disclosure; Page 36; 36pp; English.  
 XX  
 CC The invention relates to a novel human ion channel polynucleotide that  
 CC shares structural similarity with voltage-gated potassium channel  
 CC proteins. The activity of the protein of the invention may be described  
 CC as neuroprotective. The protein of the invention is useful in  
 CC therapeutic, diagnostic and pharmacogenomic applications, for example to  
 CC identify mutations associated with a particular disease, as a diagnostic  
 CC or prognostic assay, or in gene therapy. The protein of the invention has  
 CC been found to be expressed in human foetal brain, brain, cerebellum,  
 CC pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal

CC	liver, liver, testis, thyroid, salivary gland, stomach, skeletal muscle,
CC	heart, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo,
CC	adenocarcinoma and osteosarcoma cells. The current sequence represents
CC	the human voltage-gated potassium channel-like protein encoding DNA
CC	sequence
XX	
SQ	Sequence 1844 BP; 314 A; 540 C; 596 G; 394 T; 0 U; 0 Other;
Query Match	
Best Local Similarity 100.0%; Score 1278; DB 6; Length 1844;	
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGACCTTCGGCGCAGCGGGCGGCGCTCGGTGCTGTGAACGTGGGGCGGCCGGTAT 60
Db	457 ATGACCTTCGGCGCAGCGGGCGGCGCTCGGTGCTGTGAACGTGGGGCGGCCGGTAT 516
Qy	61 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGCTGGCGCGCGGTGACGCGCTCAGCGC 120
Db	517 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGCTGGCGCGCGGTGACGCGCTCAGCGC 576
Qy	121 TCCCGCTCCGAGCCGAGCTCTCGAGGTGTGCAGACATACGACCCGGAGCGCAACGAG 180
Db	577 TGC CGCTCCGAGCCGAGCTCTCGAGGTGTGCAGACATACGACCCGGAGCGCAACGAG 636
Qy	181 TACTTCTTCGACCCGGCACTCGGAGCGCTTCGGCTTCATCTGCTCTACGTGCGGGCCAC 240
Db	637 TACTTCTTCGACCCGGCACTCGGAGCGCTTCGGCTTCATCTGCTCTACGTGCGGGCCAC 696
Qy	241 GGC AAGCTCGCTTTCGGCGCGCGGATGTGCGAGTCTTCTTCTTCAACAGAGATGATCTAC 300
Db	697 GGC AAGCTCGCTTTCGGCGCGCGGATGTGCGAGTCTTCTTCTTCAACAGAGATGATCTAC 756
Qy	301 TGGGGCTTGGAGGGCGCGCACTCGAGTACTGCTGCCAGCGCGCCCTCGACACCGGATG 360
Db	757 TGGGGCTTGGAGGGCGCGCACTCGAGTACTGCTGCCAGCGCGCGCTCGACACCGGATG 816
Qy	361 TCCGACACCTACACCTTTACTTCGGCCGACGAGCGGGCGTGTGGGCCCGCGACGAGCG 420
Db	817 TCCGACACCTACACCTTTACTTCGGCCGACGAGCGGGCGTGTGGGCCCGCGACGAGCG 876
Qy	421 CGCCCCGGCGGGCGAGGGCGCTCCCTCCAGGGCGCTGGCTGGAGCGCATCGCGCGGAC 480
Db	877 CGCCCCGGCGGGCGAGGGCGCTCCCTCCAGGGCGCTGGCTGGAGCGCATCGCGCGGAC 936
Qy	481 TTCAGGAGCCACGCTGCTCGCTGGCGCGCAGATCCTGGCTAGCGTTCGGTGGTTC 540
Db	937 TTCAGGAGCCACGCTGCTCGCTGGCGCGCAGATCCTGGCTAGCGTTCGGTGGTTC 996
Qy	541 GTGATCGTGTCCATGGTGTCTGTGGCGCAGCAGTTCGCCGACTGGCGCAACGCGAGCC 600
Db	997 GTGATCGTGTCCATGGTGTCTGTGGCGCAGCAGTTCGCCGACTGGCGCAACGCGAGCC 1056
Qy	601 GCCGACAAACCGACGCTGGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGGTTGG 660
Db	1057 GCCGACAAACCGACGCTGGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGGTTGG 1116
Qy	661 TTACTGCGGAGTGCATCGTGAGGTTCATTGCTCCAAAAACAAGGTGTAGTTGTCAAG 720
Db	1117 TTACTGCGGAGTGCATCGTGAGGTTCATTGCTCCAAAAACAAGGTGTAGTTGTCAAG 1176
Qy	721 AGACCCCTGAAACATCATTTGATTACTGTGCAATACGCGGTATTACATCTCTGTCTTGATG 780
Db	1177 AGACCCCTGAAACATCATTTGATTACTGTGCAATACGCGGTATTACATCTCTGTCTTGATG 1236
Qy	781 ACAGTGTTTACAGCGGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGAGGTACTT 840
Db	1237 ACAGTGTTTACAGCGGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGAGGTACTT 1296
Qy	841 AGAATGATGAGGATTTTGGTTCGATTAAGCTTCGCCGTCACTTCATTGGTCTTCAGACA 900
Db	1297 AGAATGATGAGGATTTTGGTTCGATTAAGCTTCGCCGTCACTTCATTGGTCTTCAGACA 1356
Qy	901 CTCGGTTTGACTCTCAAAACGTTGTCACCGAGAGATGTTATGTTACTTGTCTTCATTGTTG 960



03-NOV-2000; 2000US-0245904P.  
09-NOV-2000; 2000US-0247673P.  
17-NOV-2000; 2000US-0249661P.  
20-NOV-2000; 2000US-0252232P.  
01-DEC-2000; 2000US-0250790P.  
(INCY-) INCYTE GENOMICS INC.  
Tang YT, Yue H, Nguyen DB, Hafalia AJA, Elliott VS, Lu Y;  
Walia NK, Yao MG, Baughn MR, Gandhi AR, Ding L, Sanjanwala M;  
Rakumar J, Arvizu C, Gietzen KU, Lal PG, Azimzai Y, Khan FA;  
Thangavelu K, Thornton M, Lu DAM, Tribouley CM, Warren BA, Ison CH;  
Das D, Raumann BE, Policky JL, Kearney L;  
WPI: 2002-463570/49.  
P-PSDB; ABG61549.  
New transporters and ion channels (TRICH) polypeptides, useful for  
diagnosing, preventing, and treating disorders associated with an  
abnormal expression or activity of TRICH, e.g. immunological, muscular or  
renal disorders.  
Claim 5; Page 176-177; 178pp; English.  
The invention relates to human transporters and ion channels (TRICH)  
polypeptides, a naturally occurring amino acid sequence 90 % identical to  
TRICH, a biologically active fragment of TRICH or an immunogenic fragment  
of TRICH. Also included are an isolated polynucleotide encoding TRICH, a  
recombinant polynucleotide comprising a promoter sequence operably linked  
to the TRICH polynucleotide, a cell transformed with the recombinant  
polynucleotide, a transgenic organism comprising the recombinant  
polynucleotide, an isolated antibody that binds specifically to TRICH,  
and screening for compounds which bind to TRICH. The polypeptides are  
TRICH expression or are ant/agonists of TRICH. The polypeptides are  
useful for diagnosing, treating, and preventing transport neurological,  
muscle, immunological disorders (e.g. scleroderma, systemic lupus  
erythematosus, allergies), cell proliferative disorders such as cancers  
(e.g. leukemia, cervical or breast cancers), neurodegenerative disorders  
(e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.  
myotonic dystrophy, catatonias), endocrine disorders (e.g. diabetes,  
Grave's disease), gastrointestinal disorders (e.g. Crohn's disease),  
renal disorders (e.g. Good pasture's syndrome), viral, bacterial, fungal,  
parasitic, protozoal and helminthic infections, cardiovascular disorders  
(e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis) and many  
other diseases and disorders detailed in the specification. They can also  
be used in assessing the effects of exogenous compounds on the expression  
of nucleic acid and amino acid sequences of transporters and ion  
channels. TRICH or its fragments may also be used in screening for  
compounds that specifically bind to and modulate the activity of TRICH.  
The polynucleotides can be used to create knock-in humanised animals or  
transgenic animals to model human disease. The present sequence encodes a  
TRICH protein  
Sequence 2235 BP; 395 A; 657 C; 715 G; 468 T; 0 U; 0 Other;

Query Match 57.0%; Score 729; DB 6; Length 2235;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 514 ATCTGCTAGCGTGTGCGTGTGTTGTCGTGATCGTGTCCATGCTGTGCGCCAGC 573  
DB 920 ATCTGCTAGCGTGTGCGTGTGTTGTCGTGATCGTGTCCATGCTGTGCGCCAGC 979  
QY 574 AGTTTCCCGACTGGCGCAACGAGCCGCGCAACCGGAGCTGGATACCGGAGCAGG 633  
DB 980 AGTTTCCCGACTGGCGCAACGAGCCGCGCAACCGGAGCTGGATACCGGAGCAGG 1039  
QY 634 ATAATTGAAGCTATCTGCATAGTGTGTTGTCCTGCGAGTGCATGCTGAGGTTCAATTGTC 693  
DB 1040 ATAATTGAAGCTATCTGCATAGTGTGTTGTCCTGCGAGTGCATGCTGAGGTTCAATTGTC 1099  
QY 694 TCAAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAACATCATTTACTGCGCAATC 753

Db 1100 TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAACATCATTTACTTGGCAATC 1159  
QY 754 AGCCCGTATTACATCTCTGTGTTGATGACAGAGTGTTTACAGGCGAGAACTCTCAACTCCAG 813  
Db 1160 AGCCCGTATTACATCTCTGTGTTGATGACAGAGTGTTTACAGGCGAGAACTCTCAACTCCAG 1219  
QY 814 AGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT 873  
Db 1220 AGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT 1279  
QY 874 GCGCGTCACTTCACTTGGTCTTACAGACCTCGGTTGACTCTCTCAAAAGTGTGCTACCGAGAG 933  
Db 1280 GCGCGTCACTTCACTTGGTCTTACAGACCTCGGTTGACTCTCTCAAAAGTGTGCTACCGAGAG 1339  
QY 934 ATGTTATGTTACTTGTCTTCTTCTTGTGTCATCGCAATCTTTAGTGCACATTTCTCTCAG 993  
Db 1340 ATGTTATGTTACTTGTCTTCTTCTTGTGTCATCGCAATCTTTAGTGCACATTTCTCTCAG 1399  
QY 994 CTTCTTGAACATCGGCTGGACCTGGAAACATCAACAAAGGACTTTTACCAGCATTTCTGCT 1053  
Db 1400 CTTCTTGAACATCGGCTGGACCTGGAAACATCAACAAAGGACTTTTACCAGCATTTCTGCT 1459  
QY 1054 GCCTGCTGTGGTGGTATCTCTCTATGACTACAGTTGGCTATGAGATATGATCTATC 1113  
Db 1460 GCCTGCTGTGGTGGTATCTCTCTATGACTACAGTTGGCTATGAGATATGATCTATC 1519  
QY 1114 ACAGTGCTCGAAGAAATCTTGGAGGAGTTTGTGTTTCTCAGTGGAAATTTCTTATTGGCA 1173  
Db 1520 ACAGTGCTCGAAGAAATCTTGGAGGAGTTTGTGTTTCTCAGTGGAAATTTCTTATTGGCA 1579  
QY 1174 TTACCTATCACTTTTATCTACCACTAGTTTGTGAGTGTATCATGAGCTCAAGTTTGA 1233  
Db 1580 TTACCTATCACTTTTATCTACCACTAGTTTGTGAGTGTATCATGAGCTCAAGTTTGA 1639  
QY 1234 TCTGCTAGG 1242  
Db 1640 TCTGCTAGG 1648  
RESULT 5  
ABZ24711  
ID ABZ24711 standard; cDNA; 1947 BP.  
AC ABZ24711;  
DT 07-APR-2003 (first entry)  
DE Human potassium channel subunit Kv10.1 cDNA.  
KW Potassium channel; Kv10.1; human; anticonvulsant; antiarrhythmic;  
tranquillizer; cytostatic; virucide; nootropic; neuroprotective;  
epilepsy; long Qr syndrome; muscular ataxia; arrhythmia; gene therapy;  
chromosome 2p21; gene; ss.  
OS Homo sapiens.  
PH Key Location/Qualifiers  
FT CDS 596..1906  
FT /\*tag= a  
FT /note= "Human Kv10.1"  
PN WO200296944-A2.  
PD 05-DEC-2002.  
PF 31-MAY-2002; 2002WO-EP006082.  
PR 31-MAY-2001; 2001EP-00202060.  
PA (VLAA-) VLAAms INTERUNIVERSITAIR INST BIOTECHNOG.  
PI Snyders DJ, Ottschytch N, Raes A, Van Hoorick D;  
XX

DR WPI: 2003-140443/13.  
 XX P-PSDB; ABP59352.  
 PT Novel voltage-gated heterotetrameric potassium channel useful for  
 PT diagnosing, preventing and/or treating excitability disorders, comprises  
 PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.  
 XX  
 PS Claim 3; Page 50-53; 93pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding human potassium channel  
 CC subunit Kv10.1. The cDNA was obtained by PCR from a brain library. The  
 CC invention relates to the cloning and characterisation of 3 novel voltage-  
 CC gated potassium channel subunits that were identified in the human  
 CC genome: Kv6.3 (located at 16q24.1), Kv10.1 (2p21) and Kv11.1 (9p24.2).  
 CC Yeast two-hybrid and co-immunoprecipitation experiments showed that these  
 CC subunits do not form homotetrameric channels, but do form  
 CC heterotetrameric channels with Kv2.1, Kv3.1 and/or Kv5.1. Co-expression  
 CC of each of the novel subunits with Kv2.1, Kv3.1 and/or Kv5.1 results in  
 CC currents that differ from typical Kv2.1 currents. Kv6.3, Kv10.1 and  
 CC Kv11.1 alone do not reach the plasma membrane but are retained in the  
 CC endoplasmic reticulum. Co-expression with Kv2.1 results in transport to  
 CC the plasma membrane. The invention provides novel, voltage-gated  
 CC heterotetrameric potassium channels comprising Kv2.1, Kv3.1, Kv5.1,  
 CC Kv6.3, Kv10.1 or Kv11.1. These are useful for identifying a molecule that  
 CC increases or decreases ion flux through the potassium channel. Nucleic  
 CC acids encoding the heterotetrameric potassium channels are used in gene  
 CC therapy to prevent or treat congenital or acquired excitability disorders  
 CC including epilepsy, long QT syndrome, muscular ataxia, arrhythmia (all  
 CC claimed), as well as hyperactivity disorders, mental disorders, mood  
 CC disorders, behavioural disorders, anxiety disorders, hypokalaemia,  
 CC periodic paralysis, spasticity disorders, myotonia and paramyotonia. The  
 CC nucleic acids can be used to transfect cells. For example, stem cells are  
 CC used in ex vivo procedures for cell transfection and gene therapy. The  
 CC nucleic acids are also useful in diagnosis, and in the creation of  
 CC transgenic or knockout animals  
 XX  
 SQ Sequence 1947 BP; 324 A; 596 C; 644 G; 383 T; 0 U; 0 Other;  
 Query Match 50.6%; Score 647; DB 7; Length 1947;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-313;  
 Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 GGATAATTGAGCTACTGCATAGTTGGTTGCTACTCCGAGTGCATCGAGGTCATTG 691  
 DB 1260 GGATAATTGAGCTACTGCATAGTTGGTTGCTACTCCGAGTGCATCGAGGTCATTG 1319  
 QY 692 TCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAA 751  
 DB 1320 TCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAA 1379  
 QY 752 TCACGGCGATTACATCTCTGTTGATGACAGTGTTCACAGCGGAGACTCTCAACTCC 811  
 DB 1380 TCACGGCGATTACATCTCTGTTGATGACAGTGTTCACAGCGGAGACTCTCAACTCC 1439  
 QY 812 ACAGGGCTGGAGTCACCTTGGAGGTACTTAGATGATGAGGATTTTGGGTGATTAGC 871  
 DB 1440 ACAGGGCTGGAGTCACCTTGGAGGTACTTAGATGATGAGGATTTTGGGTGATTAGC 1499  
 QY 872 TTGCGCGTCACTTCAATGGTCTTCAGACACTCGGTTGATCTCAAAACGTTGCTACCGAG 931  
 DB 1500 TTGCGCGTCACTTCAATGGTCTTCAGACACTCGGTTGATCTCAAAACGTTGCTACCGAG 1559  
 QY 932 AGATGGTTAGTTTACTTGTCTTCAATTTGTTGCCATGCAATCTTTAGTGACATTTCTC 991  
 DB 1560 AGATGGTTAGTTTACTTGTCTTCAATTTGTTGCCATGCAATCTTTAGTGACATTTCTC 1619  
 QY 992 AGCTTCTGAAACATGGGCTGGACCTGGAACATTCACAAAGACATTTACCAGCATTCCTG 1051  
 DB 1620 AGCTTCTGAAACATGGGCTGGACCTGGAACATTCACAAAGACATTTACCAGCATTCCTG 1679  
 QY 1052 CTGCTGCTGGTGGGTGATTATCTCTATGACTACAGTGTGGCTATGGAGATGATGATCTTA 1111  
 DB 1680 CTGCTGCTGGTGGGTGATTATCTCTATGACTACAGTGTGGCTATGGAGATGATGATCTTA 1739

QY 1112 TCACAGTGCCTGGAGAAATTTCTGGAGGAGTTTGTGTGTCAGTGAATTTCTTATTGG 1171  
 DB 1740 TCACAGTGCCTGGAGAAATTTCTGGAGGAGTTTGTGTGTCAGTGAATTTCTTATTGG 1799  
 QY 1172 CATTACCTATCACATTTTATCTACCATAGCTTTGTGCAAGTGTATCATGAGCTCAAGTTTA 1231  
 DB 1800 CATTACCTATCACATTTTATCTACCATAGCTTTGTGCAAGTGTATCATGAGCTCAAGTTTA 1859  
 QY 1232 GATCTGTAGTATAGTAGGAGGCTCTCCACTGAATTCCTGAATTA 1278  
 DB 1860 GATCTGTAGTATAGTAGGAGGCTCTCCACTGAATTCCTGAATTA 1906  
 RESULT 6  
 ID ADD01447 standard; cDNA; 5174 BP.  
 AC ADD01447;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human TCHI36 cDNA sequence.  
 XX  
 KW ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;  
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
 KW cytoskeletal; antisthmatic; antiarthritic; cerebroprotective;  
 KW antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;  
 KW glucose transporter; potassium ion channel protein; diabetes;  
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;  
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;  
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;  
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;  
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.  
 OS Homo sapiens.  
 XX  
 PN WO2003054190-A1.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 19-DEC-2002; 2002WO-JP013290.  
 XX  
 PR 21-DEC-2001; 2001JP-00389361.  
 PR 25-DEC-2001; 2001JP-00392577.  
 PR 26-DEC-2001; 2001JP-00394947.  
 PR 26-DEC-2001; 2001JP-00395467.  
 PR 06-FEB-2002; 2002JP-00030010.  
 PR 08-FEB-2002; 2002JP-00033095.  
 PR 06-JUN-2002; 2002JP-00165336.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Nakanishi A, Sagiya Y, Uno Y;  
 XX  
 DR WPI; 2003-541817/51.  
 XX  
 PT Glucose transporter TCH099, vesicular glutamate transporter TCHI177 and  
 PT potassium channel protein TCHI36 and DNA encoding them for diagnosis,  
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and  
 PT digestive disorders.  
 XX  
 PS Claim 62; SEQ ID NO 83; 221pp; Japanese.  
 XX  
 CC The invention relates to a novel glucose transporter TCH099, vesicular  
 CC glutamate transporter TCHI177 and voltage-dependent potassium ion channel  
 CC protein TCHI36. The sequences are useful in the treatment, prevention and  
 CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,  
 CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,



CC gastritis, ileitis and rectal inflammation), inflammatory diseases,  
CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,  
CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as  
CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and  
CC atopic dermatitis), circulatory disorders (such as heart failure), cancer  
CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,  
CC pancreas, bladder, breast, fallopian tubes or colon), central nervous  
CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and  
CC secretory disorders (such as hyperprolactinemia and Cushing's disease). This  
CC sequence represents the cDNA sequence for the novel human voltage-gated  
XX potassium ion channel protein TCH136.  
SQ Sequence 5174 BP; 1335 A; 1139 C; 1257 G; 1443 T; 0 U; 0 Other;  
Query Match 50.6%; Score 647; DB 9; Length 5174;  
Best Local Similarity 100.0%; Pred. No. 2.9e-313; Indels 0; Gaps 0;  
Matches 647; Conservative 0; Mismatches 0;  
QY 632 GGATAATTGAAGCTATCTGATAGTGGTGGTTCACATGCCGAGTGCATCGTGGATTTCATTG 691  
Db 1149 GGATAATTGAAGCTATCTGATAGTGGTGGTTCACATGCCGAGTGCATCGTGGATTTCATTG 1208  
QY 692 TCTCCAAAACAAAGTGTGAGTTGTTCAGAGACCCCTGAACATCATTTACTTACGGCAA 751  
Db 1209 TCTCCAAAACAAAGTGTGAGTTGTTCAGAGACCCCTGAACATCATTTACTTACGGCAA 1268  
QY 752 TCACGCGGATTTACATCTCTGTGTTGATGACAGTCTTTACAGGCGAGAACTCTCAACTCC 811  
Db 1269 TCACGCGGATTTACATCTCTGTGTTGATGACAGTCTTTACAGGCGAGAACTCTCAACTCC 1328  
QY 812 AGAGGCGTGGATGACCTTGAGGGTACTTAGAATGATGAGGATTTTGGTGATTAAGC 871  
Db 1329 AGAGGCGTGGATGACCTTGAGGGTACTTAGAATGATGAGGATTTTGGTGATTAAGC 1388  
QY 872 TTGCCCGTCACTTTCATTTGTTCTTCAGACACTCGGTTTGAATCTCAAAAGTGTCTACCCAG 931  
Db 1389 TTGCCCGTCACTTTCATTTGTTCTTCAGACACTCGGTTTGAATCTCAAAAGTGTCTACCCAG 1448  
QY 932 AGATGTTATGTTACTTGTCTTCAATTTGTTGGTCAATGCAATCTTTAGTGCATTTCTC 991  
Db 1449 AGATGTTATGTTACTTGTCTTCAATTTGTTGGTCAATGCAATCTTTAGTGCATTTCTC 1508  
QY 992 AGCTCTTCAACATGGCTGGACCTGGAAACATCAACAGGACATTTACCGATTCCTG 1051  
Db 1509 AGCTCTTCAACATGGCTGGACCTGGAAACATCAACAGGACATTTACCGATTCCTG 1568  
QY 1052 CTGCTGCTGCTGGTGGTATTATCTCTATGACATACAGTTGGCTATGGAGATGATATCCTTA 1111  
Db 1569 CTGCTGCTGCTGGTGGTATTATCTCTATGACATACAGTTGGCTATGGAGATGATATCCTTA 1628  
QY 1112 TCACAGTGCCTGGAGAAATCTTGGAGGAGTTTGTGTGCTAGTGAATTTCTATTGG 1171  
Db 1629 TCACAGTGCCTGGAGAAATCTTGGAGGAGTTTGTGTGCTAGTGAATTTCTATTGG 1688  
QY 1172 CATTACTATCACTTTTATCTACCATAGCTTTGTGAGTGGTATCATGAGCTCAAGTTTA 1231  
Db 1689 CATTACTATCACTTTTATCTACCATAGCTTTGTGAGTGGTATCATGAGCTCAAGTTTA 1748  
QY 1232 GATCTCTAGGTATAGTAGAGCCTCTCCATGAATTCCTGAATTA 1278  
Db 1749 GATCTCTAGGTATAGTAGAGCCTCTCCATGAATTCCTGAATTA 1795  
RESULT 7  
ADD01427  
ID ADD01427 standard; DNA; 1308 BP.  
XX  
AC ADD01427;  
XX  
DT 01-JAN-2004 (first entry)  
XX Human TCH136 coding sequence.

XX ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;  
XX neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
XX cytoskeletal; antiasthmatic; antiarthritic; cerebroprotective;  
XX antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;  
XX glucose transporter; potassium ion channel protein; diabetes;  
XX hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
XX colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
XX sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;  
XX meningitis; hepatitis; myocarditis; asthma; immune disorder;  
XX multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
XX allergy; hay fever; allergic rhinitis; anaphylactic shock;  
XX atopic dermatitis; circulatory disorder; heart failure; cancer;  
XX Alzheimer's disease; Parkinson's disease; schizophrenia;  
XX hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1.1308  
FT CDS /\*tag= a  
FT /product= "human TCH136 protein"  
FT /function= "voltage-dependent potassium ion channel"  
PN W02003054190-A1.  
PD 03-JUL-2003.  
XX 19-DEC-2002; 2002WO-JP013290.  
XX 21-DEC-2001; 2001JP-00389361.  
XX 25-DEC-2001; 2001JP-00392577.  
XX 26-DEC-2001; 2001JP-00394947.  
XX 06-FEB-2001; 2001JP-00395467.  
XX 06-FEB-2002; 2002JP-00030010.  
XX 08-FEB-2002; 2002JP-00030095.  
XX 06-JUN-2002; 2002JP-00165336.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Nakanishi A, Sagiya Y, Uno Y;  
FI WPI; 2003-541817/51.  
DR P-PSDB; ADD01426.  
XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and  
PT potassium channel protein TCH136 and DNA encoding them for diagnosis,  
PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and  
PT digestive disorders.  
XX Claim 62; SEQ ID NO 63; 221pp; Japanese.  
XX The invention relates to a novel glucose transporter TCH099, vesicular  
CC glutamate transporter TCH177 and voltage-dependent potassium ion channel  
CC protein TCH136. The sequences are useful in the treatment, prevention and  
CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,  
CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,  
CC gastritis, ileitis and rectal inflammation), inflammatory diseases,  
CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,  
CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as  
CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),  
CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and  
CC atopic dermatitis), circulatory disorders (such as heart failure), cancer  
CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,  
CC pancreas, bladder, breast, fallopian tubes or colon), central nervous  
CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and  
CC secretory disorders (such as hyperprolactinemia and Cushing's disease). This  
CC sequence represents the coding sequence for the novel human voltage-gated  
XX potassium ion channel protein TCH136.  
SQ Sequence 1308 BP; 238 A; 362 C; 389 G; 319 T; 0 U; 0 Other;  
Query Match 50.4%; Score 644; DB 9; Length 1308;



Best Local Similarity 100.0%; Pred. No. 9.3e-312;

Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	632	GGATAATTGAAGCTATCTGATAGTTGGTTCTACTGCGAGTGCATCGTGGAGTTTCATTTG	691
Db	665	GGATAATTGAAGCTATCTGATAGTTGGTTCTACTGCGAGTGCATCGTGGAGTTTCATTTG	724
QY	692	TCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAACATCATTTGATTTACTGGCAA	751
Db	725	TCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAACATCATTTGATTTACTGGCAA	784
QY	752	TCACGCGTATTACATCTCTGCTGTGATGACAGTGTTCACGCGAGAACTCTCAACTCC	811
Db	785	TCACGCGTATTACATCTCTGCTGTGATGACAGTGTTCACGCGAGAACTCTCAACTCC	844
QY	812	AGAGGGCTGGAGTCACTCTGAGGTTACTTAGAATGATGAGGATTTTTTGGGTGATTAAGC	871
Db	845	AGAGGGCTGGAGTCACTCTGAGGTTACTTAGAATGATGAGGATTTTTTGGGTGATTAAGC	904
QY	872	TTGCGCGTCACTTCACTGCTTTCAGACACTCGTTTGACTCTCAACCTTGGTACCGAG	931
Db	905	TTGCGCGTCACTTCACTGCTTTCAGACACTCGTTTGACTCTCAACCTTGGTACCGAG	964
QY	932	AGATGGTATTGTTACTTGTCTTCAATTTGTTGCCATGGCAATCTTTAGTGCACTTTCTC	991
Db	965	AGATGGTATTGTTACTTGTCTTCAATTTGTTGCCATGGCAATCTTTAGTGCACTTTCTC	1024
QY	992	AGCTTCTTGAACATGGGCTGGACCTGGAACATCCAAAGAGCTTTACAGATTCCTG	1051
Db	1025	AGCTTCTTGAACATGGGCTGGACCTGGAACATCCAAAGAGCTTTACAGATTCCTG	1084
QY	1052	CTGCTGCTGGTGGTGAATTTCTATGACTACAGTGGCTATGGAGATGATGATCTTA	1111
Db	1085	CTGCTGCTGGTGGTGAATTTCTATGACTACAGTGGCTATGGAGATGATGATCTTA	1144
QY	1112	TCACAGTGGCTGGAAGAATTTCTTGGAGGATTTGTTGTCAGTGGAATTTCTTATTTG	1171
Db	1145	TCACAGTGGCTGGAAGAATTTCTTGGAGGATTTGTTGTCAGTGGAATTTCTTATTTG	1204
QY	1172	CATTACTATCACTTTTACTACATAGCTTTGTCAGTGGTATCATGAGCTCAAGTTTA	1231
Db	1205	CATTACTATCACTTTTACTACATAGCTTTGTCAGTGGTATCATGAGCTCAAGTTTA	1264
QY	1232	GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAAATTCCTGTAAT	1275
Db	1265	GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAAATTCCTGTAAT	1308

RESULT 8

ABX72192  
ID ABX72192 standard; cdna; 1651 BP.

AC ABX72192;

XX ABX72192;

DT 03-JUN-2003 (first entry)

XX Human NOVX polynucleotide #23.

Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD; hypertension; congenital heart defect; aortic stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arteriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD; tuberculous sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; haemophilia; hypercoagulation; Crohn's disease; cancer.

OS Homo sapiens.

XX WO200281498-A2.

PN 17-OCT-2002.

XX

PF	03-APR-2002;	2002WO-US010780.
XX	03-APR-2001;	2001US-0281086P.
PR	03-APR-2001;	2001US-0281136P.
PR	05-APR-2001;	2001US-0281863P.
PR	05-APR-2001;	2001US-0281906P.
PR	06-APR-2001;	2001US-0282020P.
PR	10-APR-2001;	2001US-0282930P.
PR	10-APR-2001;	2001US-0282934P.
PR	12-APR-2001;	2001US-0283512P.
PR	13-APR-2001;	2001US-0283710P.
PR	17-APR-2001;	2001US-0284234P.
PR	19-APR-2001;	2001US-0285325P.
PR	20-APR-2001;	2001US-0285381P.
PR	20-APR-2001;	2001US-0285609P.
PR	23-APR-2001;	2001US-0285748P.
PR	23-APR-2001;	2001US-0285890P.
PR	24-APR-2001;	2001US-0286068P.
PR	25-APR-2001;	2001US-0286292P.
PR	27-APR-2001;	2001US-0287213P.
PR	02-MAY-2001;	2001US-0288257P.
PR	29-MAY-2001;	2001US-0294164P.
PR	30-MAY-2001;	2001US-0294484P.
PR	18-JUN-2001;	2001US-0298952P.
PR	19-JUN-2001;	2001US-0299237P.
PR	19-JUN-2001;	2001US-0299276P.
PR	12-SEP-2001;	2001US-0318750P.
PR	25-SEP-2001;	2001US-0324800P.
PR	25-SEP-2001;	2001US-0324802P.
PR	27-SEP-2001;	2001US-0325684P.
PR	17-OCT-2001;	2001US-0330143P.
PR	14-NOV-2001;	2001US-0332131P.
PR	14-NOV-2001;	2001US-0332240P.
PR	14-NOV-2001;	2001US-0332779P.
PR	21-NOV-2001;	2001US-0332115P.
PR	04-DEC-2001;	2001US-0337621P.
PR	03-JAN-2002;	2002US-0345783P.
PR	16-JAN-2002;	2002US-0350251P.
PR	02-APR-2002;	2002US-00114270.

(CURA-) CURAGEN CORP.

Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA, Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD; Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlach V; Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W; Anderson DW, Leite MM, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; Ellerman K;

WPI; 2003-046858/04.  
P-PSDB; ABUS4564.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 17; Page 136; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, aortic stenosis, atrial septal defect (ASD), congenital heart defects, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABX72170-ABX72275 represent human NOVX polynucleotides of the invention

XX

SQ	Sequence 1651 BP; 292 A; 476 C; 510 G; 373 T; 0 U; 0 Other;	
Query Match	48.0%; Score 613; DB 7; Length 1651;	
Best Local Similarity	100.0%; Pred. No. 3.1e-296;	
Matches 613; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	630 CAGGATAATTGAAGCTATCTGCATAGGTGGTTCTACTCCGAGTGCATCGTGGAGTTTCAT	689
DB	792 CAGGATAATTGAAGCTATCTGCATAGGTGGTTCTACTCCGAGTGCATCGTGGAGTTTCAT	851
QY	690 TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGGAACATCATTTGATTTACTGGC	749
DB	852 TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGGAACATCATTTGATTTACTGGC	911
QY	750 ATACGCGGTATTACATCTCTGCTTGTGATGACAGTGTGTACAGCGAGAACTCTCAACT	809
DB	912 ATACGCGGTATTACATCTCTGCTTGTGATGACAGTGTGTACAGCGAGAACTCTCAACT	971
QY	810 CCAGAGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGTGGATTAA	869
DB	972 CCAGAGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGTGGATTAA	1031
QY	870 GCTTCCCGTCACTTCATTTGTTTCCAGACATCTGGTTGACTCTCAACGTTGCTACCG	929
DB	1032 GCTTCCCGTCACTTCATTTGTTTCCAGACATCTGGTTGACTCTCAACGTTGCTACCG	1091
QY	930 AGAGATGGTTATGTATCTTCTTCAATTTGTTGCTTGGCAATCTTTAGTGCACTTTC	989
DB	1092 AGAGATGGTTATGTATCTTCTTCAATTTGTTGCTTGGCAATCTTTAGTGCACTTTC	1151
QY	990 TCAGCTTCTTGAACATGGCTGGAGCTGGAAACATCCCAAGAGACTTTACAGCAATTC	1049
DB	1152 TCAGCTTCTTGAACATGGCTGGAGCTGGAAACATCCCAAGAGACTTTACAGCAATTC	1211
QY	1050 TGTCTGCTGCTGGTGGTATATCTCTATGACTACAGTTGGCTATGAGATATGATCC	1109
DB	1212 TGTCTGCTGCTGGTGGTATATCTCTATGACTACAGTTGGCTATGAGATATGATCC	1271
QY	1110 TATCAGTGGCTGGAAGAAATCTTGGAGAGTTTGTGTGTGAGTGAATTTGTTCTATT	1169
DB	1272 TATCAGTGGCTGGAAGAAATCTTGGAGAGTTTGTGTGTGAGTGAATTTGTTCTATT	1331
QY	1170 GCATTACTACTTATCTTATACATAGCTTGTGAGTGTGATGAGTCAAGTTCAAGTT	1229
DB	1332 GCATTACTACTTATCTTATACATAGCTTGTGAGTGTGATGAGTCAAGTTCAAGTT	1391
QY	1230 TAGATCTGCTAGG 1242	
DB	1392 TAGATCTGCTAGG 1404	
RESULT 9		
ID	ABK27494	
XX	ABK27494 standard; cDNA; 461 BP.	
XX	ABK27494;	
XX		
DT	09-APR-2002 (first entry)	
XX		
DE	DNA encoding novel human ion channel protein #25.	
XX		
KW	Human; ion channel; anti-HIV; analgesic; cytostatic; antidiabetic;	
KW	anorectic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant;	
KW	antiatherosclerotic; neuroleptic; antimigraine; antiparkinsonian;	
KW	tranquilliser; antidepressant; neuroprotective; anticonvulsant; pain;	
KW	antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;	
KW	psychiatric disorder; gene therapy; asthma; traumatic brain injury;	
KW	human immunodeficiency virus; HIV-1; HIV-2; cancer; diabetes; anorexia;	
KW	myocardial infarction; Parkinson's disease; schizophrenia; anxiety;	
KW	dementia; Huntington's disease; thyroid disorder; inflammation;	
KW	autoimmune disorder; hormonal disorder; renal failure; psoriasis;	
KW	movement disorder; gene; ss.	

XX	Homo sapiens.	
OS		
FN	W0200185788-A2.	
XX		
PD	15-NOV-2001.	
XX		
PF		
XX	10-MAY-2001; 2001WO-US014965.	
PR	10-MAY-2000; 2000US-0203305P.	
PR	23-MAY-2000; 2000US-0206526P.	
PR	25-MAY-2000; 2000US-0207033P.	
PR	25-MAY-2000; 2000US-0207092P.	
PR	25-MAY-2000; 2000US-0207093P.	
PR	07-JUL-2000; 2000US-0216893P.	
PR	04-AUG-2000; 2000US-0223245P.	
PR	04-OCT-2000; 2000US-0237873P.	
XX		
PA	(PHAA ) PHARMACIA & UPJOHN CO.	
XX		
PI	Roberts SL, Benjamin CW, Karnovsky AM, Ruble CL;	
XX		
DR	WPI; 2002-062237/08.	
DR	P-PSDB; AAU81345.	
XX		
PT	New polynucleotied, useful for identifying ion channel activity	
PT	modulators that are used for treating Parkinson's disease, schizophrenia,	
PT	migraine, anxiety, manic depression, encodes the ion channel polypeptide.	
XX		
PS	Claim 1; Page 86; 172pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid molecule (I) which	
CC	encodes a novel ion channel protein, ion-x (ii). The nucleic acid,	
CC	protein and antibody are useful for identifying a compound which binds a	
CC	nucleic acid molecule encoding ion-x. These are useful for treatment of a	
CC	neurological or psychiatric disorder which modulates ligand binding to	
CC	ion-x in neurons of the mammal; in gene therapy to restore ion-x activity	
CC	in certain disease states; for treating asthma, traumatic brain injury,	
CC	etc; modulators of ion-x activity or expression are useful for treating	
CC	diseases such as viral infections caused by human immunodeficiency virus	
CC	(HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,	
CC	hypotension, hypertension, thrombosis, myocardial infarction,	
CC	cardiomyopathies, atherosclerosis, Parkinson's disease, schizophrenia,	
CC	migraine, anxiety, manic depression, dementia, Huntington's disease,	
CC	thyroid disorders, inflammatory conditions, rheumatoid arthritis, and	
CC	autoimmune disorders, hormonal disorders, renal failure, psoriasis, and	
CC	movement disorders. ABK27470-ABK27517 represent human ion channel protein	
CC	coding sequences and PCR primers of the invention	
XX		
SQ	Sequence 461 BP; 109 A; 93 C; 98 G; 161 T; 0 U; 0 Other;	
Query Match	27.2%; Score 347; DB 6; Length 461;	
Best Local Similarity	100.0%; Pred. No. 4.6e-163;	
Matches 347; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	932 AGATGGTTATGTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC	991
DB	49 AGATGGTTATGTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC	108
QY	992 AGCTTCTTGAACATGGGCTGGACCTGGAAACATCCCAAGAGACTTTACCAAGATTCCTG	1051
DB	109 AGCTTCTTGAACATGGGCTGGACCTGGAAACATCCCAAGAGACTTTACCAAGATTCCTG	168
QY	1052 CTGCTCTGCTGGTGGTGAATTTCTTATGACTACAGTTGGCTATGGAGATATGATCCTA	1111
DB	169 CTGCTCTGCTGGTGGTGAATTTCTTATGACTACAGTTGGCTATGGAGATATGATCCTA	228
QY	1112 TCACAGTGCCTGGAAGAAATCTTGGAGAGTTTGTGTGTGTCAGTGGAAATTTCTATTGG	1171
DB	229 TCACAGTGCCTGGAAGAAATCTTGGAGAGTTTGTGTGTGTCAGTGGAAATTTCTATTGG	288
QY	1172 CATTAACCTATCACTTTTATCTTACCATAGCTTTGTGCACTGTTTATCATGACCTCAAGTTA	1231

Db 289 CATTACTATCACTTTTATCTACCATAGCTTTGTGAGTGTATCATGAGCTCAAGTTTA 348  
QY 1232 GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTCGAATTAA 1278  
Db 349 GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTCGAATTAA 395

RESULT 10  
ABX91965/c  
ID ABX91965 standard; cDNA; 777 BP.  
XX AC ABX91965;  
XX  
DT 08-MAY-2003 (first entry)  
XX  
DE Lung specific nucleic acid (LSNA) #7.  
XX  
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;  
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;  
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200268633-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 21-NOV-2001; 2001WO-US043612.  
XX  
PR 22-NOV-2000; 2000US-0252500P.  
XX  
PA (DIAD-) DIADEXUS INC.  
XX  
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;  
XX  
DR WPI; 2002-713376/77.  
XX  
XX New isolated human nucleic acid molecule and polypeptide, useful for  
PT identifying, diagnosing, monitoring, staging, imaging and treating lung  
PT cancer and non-cancerous diseases of the lung.  
XX  
PS Claim 1; Page 163-164; 389pp; English.  
XX  
XX The invention describes an isolated human nucleic acid (I) encoding any  
CC of 120-1533 residue amino acid sequences (S1), given in the  
CC specification, comprising any of 164 179-12421 base pair sequences (S2),  
CC given in the specification. The methods and compositions of the present  
CC invention are useful for identifying, diagnosing, monitoring, staging,  
CC imaging and treating lung cancer and non-cancerous diseases of the lung.  
CC They are also used for identifying lung tissue, monitoring and  
CC identifying and/or designing antagonists of the polypeptide of the  
CC invention, gene therapy, production of transgenic animals and production  
CC of engineered lung tissue for treatment and research. This sequence  
CC encodes a lung specific nucleic acid  
XX  
SQ Sequence 777 BP; 250 A; 162 C; 158 G; 207 T; 0 U; 0 Other;  
Query Match 25.9%; Score 331; DB 6; Length 777;  
Best Local Similarity 100.0%; Pred. No. 4.7e-155;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 948 TGCCTTCATTGGTGGCCATCTTTAGTCACATCTTCTCAGCTTCTTGACATGG 1007  
Db 662 TGCCTTCATTGGTGGCCATCTTTAGTCACATCTTCTCAGCTTCTTGACATGG 603  
QY 1008 GCTGGACCTGGAAACATCCAAAGGACTTTACCAGCATTCCTGCTGCTGTGGGT 1067  
Db 602 GCTGGACCTGGAAACATCCAAAGGACTTTACCAGCATTCCTGCTGCTGTGGGT 543  
QY 1068 GATTATCTCTATGACTACAGTTGGCTATGAGATATGATATCCTATCAGAGTCCCTGGAAG 1127  
Db 542 GATTATCTCTATGACTACAGTTGGCTATGAGATATGATATCCTATCAGAGTCCCTGGAAG 483

QY 1128 AATCTTGGAGAGTTTGTGTGTGTCAGTGGAAATTTCTATTGGCATTACCTACCTTT 1187  
Db 482 AATCTTGGAGAGTTTGTGTGTGTCAGTGGAAATTTCTATTGGCATTACCTACCTTT 423  
QY 1188 TATCTACCATAGCTTTGTGAGTGTATCATGAGTCAAGTTTAGATCTCTAGGTATAG 1247  
Db 422 TATCTACCATAGCTTTGTGAGTGTATCATGAGTCAAGTTTAGATCTCTAGGTATAG 363

QY 1248 TAGGAGCTCTCCACTGAATTCCTGAATTAA 1278  
Db 362 TAGGAGCTCTCCACTGAATTCCTGAATTAA 332

RESULT 11  
ABX91966  
ID ABX91966 standard; cDNA; 911 BP.  
XX AC ABX91966;  
XX  
DT 08-MAY-2003 (first entry)  
XX  
DE Lung specific nucleic acid (LSNA) #8.  
XX  
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;  
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;  
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200268633-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 21-NOV-2001; 2001WO-US043612.  
XX  
PR 22-NOV-2000; 2000US-0252500P.  
XX  
PA (DIAD-) DIADEXUS INC.  
XX  
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;  
XX  
DR WPI; 2002-713376/77.  
XX  
XX New isolated human nucleic acid molecule and polypeptide, useful for  
PT identifying, diagnosing, monitoring, staging, imaging and treating lung  
PT cancer and non-cancerous diseases of the lung.  
XX  
PS Claim 1; Page 164; 389pp; English.  
XX  
XX The invention describes an isolated human nucleic acid (I) encoding any  
CC of 120-1533 residue amino acid sequences (S1), given in the  
CC specification, comprising any of 164 179-12421 base pair sequences (S2),  
CC given in the specification. The methods and compositions of the present  
CC invention are useful for identifying, diagnosing, monitoring, staging,  
CC imaging and treating lung cancer and non-cancerous diseases of the lung.  
CC They are also used for identifying lung tissue, monitoring and  
CC identifying and/or designing antagonists of the polypeptide of the  
CC invention, gene therapy, production of transgenic animals and production  
CC of engineered lung tissue for treatment and research. This sequence  
CC encodes a lung specific nucleic acid  
XX  
SQ Sequence 911 BP; 249 A; 168 C; 181 G; 313 T; 0 U; 0 Other;  
Query Match 17.0%; Score 217; DB 6; Length 911;  
Best Local Similarity 100.0%; Pred. No. 5.6e-98;  
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1062 GTGGGTGATTATCTCTATGACTACAGTTGGCTATGGAGATATGATCCTATCAGTGCC 1121  
Db 229 GTGGGTGATTATCTCTATGACTACAGTTGGCTATGGAGATATGATCCTATCAGTGCC 288  
QY 1122 TGAAGAAATCTTGGAGAGTGTGTGTGTGTCAGTGGAAATTTCTATTGGCATTACCTAT 1181

Db 289 TGAAGAATCTTGGAGGAGTTTGTGTCAGTGAATTTGTTCTATTGGCATACCTAT 348  
QY 1182 CACTTTTATCTACCATAGCTTTGTGTCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAG 1241  
Db 349 CACTTTTATCTACCATAGCTTTGTGTCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAG 408  
QY 1242 GTATAGTAGGAGCTCTCCACTGAATTTCTGAAATTAA 1278  
Db 409 GTATAGTAGGAGCTCTCCACTGAATTTCTGAAATTAA 445  
RESULT 12  
ABZ24716  
ID ABZ24716 standard; cDNA; 5775 BP.  
XX  
AC ABZ24716;  
XX  
DT 07-APR-2003 (first entry)  
DE Murine potassium channel subunit Kv10.1 - flag sequence.  
XX  
KW Potassium channel; Kv10.1; mouse; transgenic mouse; gene; ss.  
XX  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT misc\_feature 3424..4749  
FT /tag= "a"  
FT /note= "flag"  
XX  
PN WO200296944-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 31-MAY-2002; 2002WO-EP006082.  
XX  
PR 31-MAY-2001; 2001EP-00202060.  
XX  
PA (VLAAS) VLAAS INTERUNIVERSITAIR INST BIOTECHNOG.  
XX  
PI Snyders DJ, Ottechytsch N, Raes A, Van Hoorick D;  
XX  
XX WPI; 2003-140443/13.  
DR  
PT Novel voltage-gated heterotetrameric potassium channel useful for  
PT diagnosing, preventing and/or treating excitability disorders, comprises  
PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.  
XX  
PS Example; Page 80-82; 93pp; English.  
XX  
CC The present sequence is that of a construct used in the creation of a  
CC potassium channel subunit Kv10.1 transgenic mouse. In an example from the  
CC invention, the construct was microinjected into the pronucleus of a one-  
CC cell embryo, and then incubated in a foster mother of the FVB/Nlco mouse  
CC strain. The invention provides novel, voltage-gated heterotetrameric  
CC potassium channels comprising Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or  
CC Kv11.1. These are useful for identifying a molecule that increases or  
CC decreases ion flux through the potassium channel (claimed). Nucleic acids  
CC encoding the heterotetrameric potassium channels are used in gene therapy  
CC to prevent or treat congenital or acquired excitability disorders  
CC including epilepsy, long QT syndrome, muscular ataxia, and arrhythmia  
CC (all claimed)  
XX  
SQ Sequence 5775 BP; 1327 A; 1530 C; 1532 G; 1386 T; 0 U; 0 Other;  
Query Match 5.6%; Score 71; DB 7; Length 5775;  
Best Local Similarity 100.0%; Pred. No. 6.8e-25;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 244 AGCTGCGTTTCGCGCGGATGTGCGAGCTCTCTTCTACAGAGATGATCTACTGG 303  
Db 3667 AAGCTGCGTTTCGCGCGGATGTGCGAGCTCTCTTCTACAGAGATGATCTACTGG 3726

QY 304 GGCTGTGAGGG 314  
Db 3727 GGCTGTGAGGG 3737  
RESULT 13  
ADD01469  
ID ADD01469 standard; cDNA; 950 BP.  
XX  
AC ADD01469;  
XX  
DT 01-JAN-2004 (first entry)  
DE Mouse TCH136 cDNA sequence fragment.  
XX  
KW ds; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;  
KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
KW cyostatic; antiasthmatic; antiarthritic; cerebrotective;  
KW antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;  
KW glucose transporter; potassium ion channel protein; diabetes;  
KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;  
KW meningitis; hepatitis; myocarditis; asthma; immune disorder;  
KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
KW allergic; hay fever; allergic rhinitis; anaphylactic shock;  
KW atopic dermatitis; circulatory disorder; heart failure; cancer;  
KW Alzheimer's disease; Parkinson's disease; schizophrenia;  
KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.  
XX  
OS Mus sp.  
XX  
PN WO2003054190-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 19-DEC-2002; 2002WO-JP013290.  
XX  
PR 21-DEC-2001; 2001JP-00389361.  
PR 25-DEC-2001; 2001JP-00392577.  
PR 26-DEC-2001; 2001JP-00394947.  
PR 26-DEC-2001; 2001JP-00395467.  
PR 06-FEB-2002; 2002JP-00030010.  
PR 08-FEB-2002; 2002JP-00033095.  
PR 06-JUN-2002; 2002JP-00165336.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Nakanishi A, Sagiya Y, Uno Y;  
XX  
XX WPI; 2003-541817/51.  
XX  
CC Glucose transporter TCH099, vesicular glutamate transporter TCH177 and  
CC potassium channel protein TCH136 and DNA encoding them for diagnosis,  
CC treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and  
CC digestive disorders.  
XX  
CC Example 21; SEQ ID NO 105; 221pp; Japanese.  
XX  
PS The invention relates to a novel glucose transporter TCH099, vesicular  
CC glutamate transporter TCH177 and voltage-dependent potassium ion channel  
CC protein TCH136. The sequences are useful in the treatment, prevention and  
CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,  
CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,  
CC gastritis, ileitis and rectal inflammation), inflammatory diseases,  
CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,  
CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as  
CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),  
CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and  
CC atopic dermatitis), circulatory disorders (such as heart failure), cancer  
CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,  
CC pancreas, bladder, breast, fallopian tubes or colon), central nervous  
CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and

CC secretory disorders (such hyperprolactinemia and Cushing's disease). This  
 CC sequence represents a fragment of the cDNA sequence for the novel mouse  
 CC voltage-dependent potassium ion channel protein TCH136.

XX  
 SQ Sequence 950 BP; 182 A; 263 C; 269 G; 230 T; 0 U; 6 Other;

Query Match 5.5%; Score 70; DB 9; Length 950;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-24;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 452 GGGCTGGCTGGAGCGCATGCGCGGACCTTCAGAGAGCCACGTCGTCGTCGGCGCGC 511  
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 Db 150 GGGCTGGCTGGAGCGCATGCGCGGACCTTCAGAGAGCCACGTCGTCGTCGGCGCGC 209

QY 512 AGATCCTGGC 521

Db 210 AGATCCTGGC 219

## RESULT 14

ABQ49122  
 ID ABQ49122 standard; DNA; 1634 BP.

XX AC ABQ49122;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35713.

XX KH Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX  
 PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX  
 CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNPs); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation

CC status of many C residues to be determined simultaneously. ABQ13410-  
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention

XX SQ Sequence 1634 BP; 212 A; 232 C; 624 G; 566 T; 0 U; 0 Other;

Query Match 2.3%; Score 29; DB 6; Length 1634;

Best Local Similarity 100.0%; Pred. No. 0.00073;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 TAGCGTTCGGTGGTGTTCGTGATCGTGT 550

|||||  
 Db 1244 TAGCGTTCGGTGGTGTTCGTGATCGTGT 1272

## RESULT 15

ABQ49123/c

ID ABQ49123 standard; DNA; 1634 BP.

XX AC ABQ49123;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35714.

XX KH Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX  
 PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX  
 CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNPs); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously. ABQ13410-  
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the

CC disclosure of the invention  
 XX  
 SQ Sequence 1634 BP; 566 A; 624 C; 232 G; 212 T; 0 U; 0 Other;  
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 Best Local Similarity 100.0%; Pred. No. 0.00073;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 522 TAGCGTGTCCGTGGTTCGTGATCGTGT 550  
 Db 391 TAGCGTGTCCGTGGTTCGTGATCGTGT 363

Search completed: April 19, 2004, 17:06:05  
 Job time : 589 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 16:49:26 ; Search time 117 Seconds  
(without alignments)  
6061.771 Million cell updates/sec

Title: US-10-016-647-1  
Perfect score: 1278  
Sequence: 1 atgaccttcggcgcgagcgg.....ccactgaattcctgaattaa 1278

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 24

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: April 19, 2004, 19:34:58  
Job time : 117 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 16:57:24 ; Search time 4632 Seconds  
(without alignments)  
9708.087 Million cell updates/sec

Title: US-10-016-647-1

Perfect score: 1278

Sequence: 1 atgaccttcggcgacggg.....ccactgaattccgtgaattaa 1278

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 37577330 seqs, 17593059518 residues

Word size : 24

Total number of hits satisfying chosen parameters: 72

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1227	96.0	3215	1	Sequence 3, Appli
4	1227	96.0	3215	1	Sequence 1, Appli
5	1227	96.0	3215	46	Sequence 1, Appli
6	840	65.3	3215	87	Sequence 47, Appli
7	834	65.3	2312	49	Sequence 1828, Ap
8	729	57.0	2235	51	Sequence 39, Appli
9	729	57.0	2405	1	Sequence 1172, Ap
10	649	50.8	695	75	Sequence 1268, Ap
11	647	50.6	2204	1	Sequence 85, Appli
12	613	48.0	1651	1	Sequence 45, Appli
13	613	48.0	1651	45	Sequence 45, Appli
14	594	46.5	594	1	Sequence 26, Appli
15	594	46.5	594	46	Sequence 26, Appli
16	594	46.5	594	87	Sequence 26, Appli
17	582	45.5	1315	79	Sequence 2448, Ap
18	562	44.0	1147	79	Sequence 2448, Ap
19	519	40.6	520	77	Sequence 1094, Ap
20	495	38.7	649	75	Sequence 392, App
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23	495	38.7	649	75	Sequence 395, App
24	495	38.7	649	75	Sequence 396, App
25	495	38.7	649	75	Sequence 397, App
26	495	38.7	649	75	Sequence 36, Appli
27	430	33.6	1317	31	Sequence 4, Appli
28	430	33.6	1317	45	Sequence 4, Appli
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32	347	27.2	461	1	Sequence 25, Appli
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34	347	27.2	461	73	Sequence 127, App
35	331	25.9	777	42	Sequence 7, Appli
36	277	21.7	355	72	Sequence 230, App
37	277	21.7	355	72	Sequence 1270, Ap
38	276	21.6	354	72	Sequence 85, Appli
39	276	21.6	354	72	Sequence 739, App
40	252	19.7	582	73	Sequence 87, Appli
41	228	17.8	1103	28	Sequence 6, Appli
42	217	17.0	911	42	Sequence 8, Appli
43	138	10.8	138	1	Sequence 28, Appli
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ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/10016647  
; GENERAL INFORMATION:  
; APPLICANT: Friddle, Carl Johan  
; APPLICANT: Hilbun, Erin  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: Novel Human Ion Channel Protein and Polynucleotides Encoding the  
; FILE REFERENCE: LEX-0284-USA  
; CURRENT APPLICATION NUMBER: US/10/016,647  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/257,932  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1278  
; TYPE: DNA  
; ORGANISM: homo sapiens

US-10-016-647-1

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DB	121	TGCGCTCCGAGCGGAGCTGCTCGAGGTGTGAGGACTACGACCGGAGCGCAAGAG	180	
QY	181	TACTTCTTCGACCGGAGCTGCTCGAGGCTTCCGGTTCATCTGTCTACGTGCGGGCAC	240	
DB	181	TACTTCTTCGACCGGAGCTGCTCGAGGCTTCCGGTTCATCTGTCTACGTGCGGGCAC	240	
QY	241	GGCAAGCTGCGCTTCGGGGCGCGGATGTGGAGCTCTCTTCTAACACGAGATGATCTAC	300	
DB	241	GGCAAGCTGCGCTTCGGGGCGCGGATGTGGAGCTCTCTTCTAACACGAGATGATCTAC	300	
QY	301	TGGGGCTTGGAGGCGGCGACCTCGAGTACTGTGCGCGCGCGCTGAGAGCCGCGATG	360	
DB	301	TGGGGCTTGGAGGCGGCGACCTCGAGTACTGTGCGCGCGCGCTGAGAGCCGCGATG	360	
QY	361	TCGACACCTACACCTTCTACTCGGCGCGAGCGCGGCTGTGGCGCGCGAGGCG	420	
DB	361	TCGACACCTACACCTTCTACTCGGCGCGAGCGCGGCTGTGGCGCGCGAGGCG	420	
QY	421	CGCCCGCGGGGCGAGGGGCTCCCTCCAGGGCTGGTGGAGCGCATCGCGCGGACC	480	
DB	421	CGCCCGCGGGGCGAGGGGCTCCCTCCAGGGCTGGTGGAGCGCATCGCGCGGACC	480	
QY	481	TTGAGGAGCGGCGGCTCGTGGCGCGGAGATCTGGCTAGCGTGTGGTGTTC	540	
DB	481	TTGAGGAGCGGCGGCTCGTGGCGCGGAGATCTGGCTAGCGTGTGGTGTTC	540	
QY	541	GTGATCGTGTCCATGTGTGTGCGCGAGACGTTGCCCGGAGCGGCGGCGGAGCC	600	
DB	541	GTGATCGTGTCCATGTGTGTGCGCGAGACGTTGCCCGGAGCGGCGGCGGAGCC	600	
QY	601	GGCCACAAACGCGAGCGTGGATGACCGGAGGAGGATTAATCAAGCTATCTCATAGGTGG	660	
DB	601	GGCCACAAACGCGAGCGTGGATGACCGGAGGAGGATTAATCAAGCTATCTCATAGGTGG	660	
QY	661	TTCACTCCGAGTGCATCGTGAAGTTCATTTCTCCAAAAACAAGTGTGAGTTGTCAAG	720	
DB	661	TTCACTCCGAGTGCATCGTGAAGTTCATTTCTCCAAAAACAAGTGTGAGTTGTCAAG	720	
QY	721	AGACCCCTGAGCATCTATTGTTTACTGGCAATCAGCGCGTATTACATCTCTGTGTGATG	780	
DB	721	AGACCCCTGAGCATCTATTGTTTACTGGCAATCAGCGCGTATTACATCTCTGTGTGATG	780	
QY	781	ACAGTGTTCAGCGGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGGGTACTT	840	
DB	781	ACAGTGTTCAGCGGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGGGTACTT	840	
QY	841	AGATGATGAGGATTTTGGGTCATTAAGCTTCCCGTCACTTCACTTGTCTTCAGACA	900	
DB	841	AGATGATGAGGATTTTGGGTCATTAAGCTTCCCGTCACTTCACTTGTCTTCAGACA	900	
QY	901	CTCGTTTGAATCTCAAAACGCTTGTACCGGAGGATGTTTATGTTACTTGTCTTCAATTTG	960	
DB	901	CTCGTTTGAATCTCAAAACGCTTGTACCGGAGGATGTTTATGTTACTTGTCTTCAATTTG	960	
QY	961	GTTCGCAATGCAATCTTTAGTGACCTTCTCAGCTTCTTGAAATGGGCTGGACCTGGAA	1020	
DB	961	GTTCGCAATGCAATCTTTAGTGACCTTCTCAGCTTCTTGAAATGGGCTGGACCTGGAA	1020	



; PRIOR APPLICATION NUMBER: US 60/306,577  
 ; PRIOR FILING DATE: 2001-07-19  
 ; NUMBER OF SEQ ID NOS: 90  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 3215  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1275)  
 ; OTHER INFORMATION:  
 PCT-US02-23407-1

Query Match 96.0%; Score 1227; DB 1; Length 3215;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGAGCTGGAAGTGGCGCGCGCGGTAT	60
Db	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGAACTGGCGCGCGCGCGGTAT	60
QY	61	TCGCTGTCCGGGAGCTGTGAAGGACTTCCCGCTGCGCGCGGTGACCGGC	120
Db	61	TCGCTGTCCGGGAGCTGTGAAGGACTTCCCGCTGCGCGCGGTGACCGGC	120
QY	121	TGGCGCTCCAGCGCGAGCTGTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	180
Db	121	TGGCGCTCCAGCGCGAGCTGTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	180
QY	181	TACTTCTTCGACCGGCACTCGGAGGCTTCGGTCTTCATCTGCTTACGTGCGCGCCAC	240
Db	181	TACTTCTTCGACCGGCACTCGGAGGCTTCGGTCTTCATCTGCTTACGTGCGCGCCAC	240
QY	241	GGCAAGTGGCTTCGGCGCGCGAGTGTGCGAGCTCTCTTTACAAAGAGATGATCTAC	300
Db	241	GGCAAGTGGCTTCGGCGCGCGAGTGTGCGAGCTCTCTTTACAAAGAGATGATCTAC	300
QY	301	TGGGGCTGAGGGCGCGACCTCGAGTACTGTGCGAGCGCGGCTCGACCGCGCATG	360
Db	301	TGGGGCTGAGGGCGCGACCTCGAGTACTGTGCGAGCGCGGCTCGACCGCGCATG	360
QY	361	TCCGACACCTTACTTCTACTGCGCGCGAGCGCGGCTGCTGGCGCGCAGCGAGCG	420
Db	361	TCCGACACCTTACTTCTACTGCGCGCGAGCGCGGCTGCTGGCGCGCAGCGAGCG	420
QY	421	CGCGCGCGGGCGCGAGCGGCTTCCCTCAGCGCTGCTGAGGCGATGCGCGCGAC	480
Db	421	CGCGCGCGGGCGCGAGCGGCTTCCCTCAGCGCTGCTGAGGCGATGCGCGCGAC	480
QY	481	TTGAGGAGCGCCACGCTGCTGCTGCGCGCGAGATCTTGGCTAGCGTGTGCTGTTTC	540
Db	481	TTGAGGAGCGCCACGCTGCTGCTGCGCGCGAGATCTTGGCTAGCGTGTGCTGTTTC	540
QY	541	GTGATCGTTCATGT	600
Db	541	GTGATCGTTCATGT	600
QY	601	GCGGACAAACCGGAGCTGATGACCGGAGCGAGTAAATTGAAGCTATCTGATAGTTGG	660
Db	601	GCGGACAAACCGGAGCTGATGACCGGAGCGAGTAAATTGAAGCTATCTGATAGTTGG	660
QY	661	TTCACTGCGGAGTGATGTGAGTTTCAATTGTCTCAAAAAACAAGTGTGAGTTGTCAAG	720
Db	661	TTCACTGCGGAGTGATGTGAGTTTCAATTGTCTCAAAAAACAAGTGTGAGTTGTCAAG	720
QY	721	AGACCCCTGAAATCATTTACTTGTGCAATTCAGCGGTATTCATCTGTGTGTGTGT	780
Db	721	AGACCCCTGAAATCATTTACTTGTGCAATTCAGCGGTATTCATCTGTGTGTGTGT	780
QY	781	ACAGTGTTTACAGGAGAACTCTCAACTCCAGGGCTGAGTCACTTGTGAGGTTACTT	840
Db	781	ACAGTGTTTACAGGAGAACTCTCAACTCCAGGGCTGAGTCACTTGTGAGGTTACTT	840

QY	841	AGAATGATGAGGATTTTTTGGGTGATTAAGCTTCCCGTCACTTTCATTGGTCTTCAGACA	900
Db	841	AGAATGATGAGGATTTTTTGGGTGATTAAGCTTCCCGTCACTTTCATTGGTCTTCAGATA	900
QY	901	CTCGGTTTGACTCTCAAACTGTTGCTACCGAGAGATGGTATGTTACTTGTCTTCAATTTGT	960
Db	901	CTCGGTTTGACTCTCAAACTGTTGCTACCGAGAGATGGTATGTTACTTGTCTTCAATTTGT	960
QY	961	GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA	1020
Db	961	GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA	1020
QY	1021	ACATCCAAAGGACTTTTACCGAGATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080
Db	1021	ACATCCAAAGGACTTTTACCGAGATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080
QY	1081	ACTCAGTTGGCTATGAGATATGATATCTATACAGTGCCTGGAAGAATCTTGGAGGA	1140
Db	1081	ACTCAGTTGGCTATGAGATATGATATCTATACAGTGCCTGGAAGAATCTTGGAGGA	1140
QY	1141	GTTTGTGTGTGCTGAGGAAATTTCTATGCGCATTTACCTTATCTATCTACCATAGC	1200
Db	1141	GTTTGTGTGTGCTGAGGAAATTTCTATGCGCATTTACCTTATCTATCTACCATAGC	1200
QY	1201	TTTGTGAGTGTATATGAGCTCAAGTTTGTAGTCTGCTAGGTATAGTAGAGCTCTCC	1260
Db	1201	TTTGTGAGTGTATATGAGCTCAAGTTTGTAGTCTGCTAGGTATAGTAGAGCTCTCC	1260
QY	1261	ACTCAATTTCTGAAATTA 1278	
Db	1261	ACTCAATTTCTGAAATTA 1278	

RESULT 4  
 US-10-199-869-1  
 ; Sequence 1, Application US/10199869  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
 ; FILE REFERENCE: D0161 NP  
 ; CURRENT APPLICATION NUMBER: US/10/199,869  
 ; PRIOR FILING DATE: 2002-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/306,577  
 ; PRIOR FILING DATE: 2001-07-19  
 ; NUMBER OF SEQ ID NOS: 90  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 3215  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1275)  
 ; OTHER INFORMATION:  
 US-10-199-869-1

Query Match 96.0%; Score 1227; DB 46; Length 3215;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGCTGAAAGTGGCGCGCGCGGTAT	60
Db	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGCTGAAAGTGGCGCGCGCGGTAT	60
QY	61	TCGCTGTCCGGGAGCTGTGAGGACTTCCCGCTGCGCGGTGAGCGGCTGCACCGC	120
Db	61	TCGCTGTCCGGGAGCTGTGAGGACTTCCCGCTGCGCGGTGAGCGGCTGCACCGC	120
QY	121	TGCGGTTCGAGCGGACGCTGCTCCAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	180
Db	121	TGCGGTTCGAGCGGACGCTGCTCCAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	180

181 TACTTTTCGACCGGCACTCGAGGCTTTCGGCTTCACTCTGCTCTAGCTGGGGCCAC 240  
Db TACTTTTCGACCGGCACTCGAGGCTTTCGGCTTCACTCTGCTCTAGCTGGGGCCAC 240  
241 GCGAGCTCGCTTCGCGCGGGGATGTGGAGCTCTCTTCTACAGAGATGATCTAC 300  
Db GCGAGCTCGCTTCGCGCGGGGATGTGGAGCTCTCTTCTACAGAGATGATCTAC 300  
301 TGGGCGCTTGGAGGCGCGCACTCGAGTACTGCTCCAGCGCGCTCTGAGACCGCATG 360  
Db TGGGCGCTTGGAGGCGCGCACTCGAGTACTGCTCCAGCGCGCTCTGAGACCGCATG 360  
361 TCGACACTACCTTCTACTTCGCGCGAGCGCGGGCTGCTGGGCGCGGACGAGCG 420  
Db TCGACACTACCTTCTACTTCGCGCGAGCGCGGGCTGCTGGGCGCGGACGAGCG 420  
421 CGCGCGCGGCGCGAGCGGCTCCCTCCAGCGCGCTGCTGGAGCGCATGCGGCGACC 480  
Db CGCGCGCGGCGCGAGCGGCTCCCTCCAGCGCGCTGCTGGAGCGCATGCGGCGACC 480  
481 TTCGAGGAGCGCGCTCGCTCGCGCGAGATCTCTGGCTAGCGTGTGGTGTTC 540  
Db TTCGAGGAGCGCGCTCGCTCGCGCGAGATCTCTGGCTAGCGTGTGGTGTTC 540  
541 GTGATCGTGTCCATCGTGTGTGCGCGAGCGCTTGGCGGCGAGCGCGCGCGCG 600  
Db GTGATCGTGTCCATCGTGTGTGCGCGAGCGCTTGGCGGCGAGCGCGCGCGCG 600  
601 GCGGCAACCGCGAGCGCTGATGACCGGAGCGAGTAAATTGAGCTATTCGATAGTTGG 660  
Db GCGGCAACCGCGAGCGCTGATGACCGGAGCGAGTAAATTGAGCTATTCGATAGTTGG 660  
661 TTCACCTGCGAGTGATCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db TTCACCTGCGAGTGATCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
721 AGACCGCTGAACTATTGATTTACTGCGCAATCGCGCTTATACATCTCTGTGTGATG 780  
Db AGACCGCTGAACTATTGATTTACTGCGCAATCGCGCTTATACATCTCTGTGTGATG 780  
781 ACAGTGTTCAGGCGAGAACTCTCAATCTCCAGAGGCTGAGTCACTTGAAGGTAATT 840  
Db ACAGTGTTCAGGCGAGAACTCTCAATCTCCAGAGGCTGAGTCACTTGAAGGTAATT 840  
841 AGAATGATGAGATTTTTTGGGTGATTAAGCTTTCAGCTTCCAGCTTCCAGCTTCC 900  
Db AGAATGATGAGATTTTTTGGGTGATTAAGCTTTCAGCTTCCAGCTTCCAGCTTCC 900  
901 CTCGGTTTGACTCTCAAGCTTGTACCGAGAGATGGTTATGTTACTTGTCTCAATTGT 960  
Db CTCGGTTTGACTCTCAAGCTTGTACCGAGAGATGGTTATGTTACTTGTCTCAATTGT 960  
961 GTTGCCATGGCACTTTTGTAGTCACTTTCTAGCTTCTTGAACATGGGCTGACCTGGA 1020  
Db GTTGCCATGGCACTTTTGTAGTCACTTTCTAGCTTCTTGAACATGGGCTGACCTGGA 1020  
1021 ACATCCAAACAGGACTTTTACAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Db ACATCCAAACAGGACTTTTACAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
1081 ACTACAGTTGGCTATGGAGATGATCTATCAGAGTCCCTGGAAGAAATTTCTGGAGA 1140  
Db ACTACAGTTGGCTATGGAGATGATCTATCAGAGTCCCTGGAAGAAATTTCTGGAGA 1140  
1141 GTTGTGTTGTGAGTGAATTTGTTCTATTGGCAATACCTATCACTTTTATCTACCATAG 1200  
Db GTTGTGTTGTGAGTGAATTTGTTCTATTGGCAATACCTATCACTTTTATCTACCATAG 1200  
1201 TTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1260  
Db TTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1260

QY 1261 ACTGAATTCCTGAATTAA 1278  
Db 1261 ACTGAATTCCTGAATTAA 1278  
RESULT 5  
US-60-306-577-1  
; Sequence 1, Application US/60306577  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
; FILE REFERENCE: D0161  
; CURRENT APPLICATION NUMBER: US/60/306,577  
; CURRENT FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3215  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1275)  
US-60-306-577-1

Query Match 96.0%; Score 1227; DB 87; Length 3215;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGACCTTCGGGCGAGCGGGCGGCTCGTGGTGTGTGAACGTGGCGCGCCCGGTAT 60  
Db 1 ATGACCTTCGGGCGAGCGGGCGGCTCGTGGTGTGTGAACGTGGCGCGCCCGGTAT 60  
QY 61 TCGGTGTCCCGGAGCTGTGAGGACTTCCGCTGCGCGCGGTGAGCGCTGACGGC 120  
Db 61 TCGGTGTCCCGGAGCTGTGAGGACTTCCGCTGCGCGCGGTGAGCGCTGACGGC 120  
QY 121 TCGCGCTCCGAGCGCGACGTGCTCGAGTGTGGAGCACTACGACCGGAGCGAACG 180  
Db 121 TCGCGCTCCGAGCGCGACGTGCTCGAGTGTGGAGCACTACGACCGGAGCGAACG 180  
QY 181 TACTTCTTCACCGGCACTCGAGGCTTTCGGCTTCACTCTGCTCTAGCTGCGGGCC 240  
Db 181 TACTTCTTCACCGGCACTCGAGGCTTTCGGCTTCACTCTGCTCTAGCTGCGGGCC 240  
QY 241 GCGAAGCTGCGCTTCGCGCGCGGATGTGGAGCTCTCTTCTACACGAGATGATCTAC 300  
Db 241 GCGAAGCTGCGCTTCGCGCGCGGATGTGGAGCTCTCTTCTACACGAGATGATCTAC 300  
QY 301 TGGGCGCTGAGGCGCGCACTCGAGTATGCTGCCAGCGCGCTCGAGCGCGCATG 360  
Db 301 TGGGCGCTGAGGCGCGCACTCGAGTATGCTGCCAGCGCGCTCGAGCGCGCATG 360  
QY 361 TCCGACACTTACTCTTCTACTCGCGCGAGCGGGCTTCCCTCCAGGCGCTGGCTGAGCGCATGCGCGGAC 420  
Db 361 TCCGACACTTACTCTTCTACTCGCGCGAGCGGGCTTCCCTCCAGGCGCTGGCTGAGCGCATGCGCGGAC 420  
QY 421 CGCGCGCGGCGCGAGCGGGCTTCCCTCCAGGCGCTGGCTGAGCGCATGCGCGGAC 480  
Db 421 CGCGCGCGGCGCGAGCGGGCTTCCCTCCAGGCGCTGGCTGAGCGCATGCGCGGAC 480  
QY 481 TTCGAGAGCGCGCACTGCTGCTGGCGCGAGTCTTGGCTAGCTGCTGGTGTTC 540  
Db 481 TTCGAGAGCGCGCACTGCTGCTGGCGCGAGTCTTGGCTAGCTGCTGGTGTTC 540  
QY 541 GTGATCGTGTCCATGTGTGTGCTGCGCGCAGACAGTTCGCCGACTGGCGCAACGCGAC 600  
Db 541 GTGATCGTGTCCATGTGTGTGCTGCGCGCAGACAGTTCGCCGACTGGCGCAACGCGAC 600  
QY 601 GCGGCAACCGGAGCTGATGACCGGAGCGAGTAAATTGAGCTATTCGATAGTTGG 660  
Db 601 GCGGCAACCGGAGCTGATGACCGGAGCGAGTAAATTGAGCTATTCGATAGTTGG 660





Db 1666 GATATGATCCATACAGTGCCTGGAAGATTCCTGGAGAGTTGTGTGTCAGTGA 1725  
QY 1159 ATTGTTCTATTGGCAATACCTATCACTTTATCTACCACTAGCTTTGTGAGTGTATCAT 1218  
Db 1726 ATTGTTCTATTGGCAATACCTATCACTTTATCTACCACTAGCTTTGTGAGTGTATCAT 1785  
QY 1219 GAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATAA 1278  
Db 1786 GAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATAA 1845  
RESULT 7  
US-10-170-235-1828  
; Sequence 1828, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; FILE REFERENCE: TRANSSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 1828  
; LENGTH: 1416  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-1828  
Query Match 65.3%; Score 834; DB 46; Length 1416;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 834; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGAAGTCCGGTGGCGGGCGGCGGCGGTAT 60  
Db 1 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGAAGTCCGGTGGCGGGCGGCGGCGGTAT 60  
QY 61 TCGCTTCGGGAGCTGCTGAAGTCCGGTGGCGGGCGGCGGCGGTGAGCGGCGGCGGCGGCGG 120  
Db 61 TCGCTTCGGGAGCTGCTGAAGTCCGGTGGCGGGCGGCGGCGGTGAGCGGCGGCGGCGGCGG 120  
QY 121 TCGCGCTTCGGGCGCAGCGGCTGCTGAGGCTGTCGAGAGTACGACGCGGCGGCGGCGGCGG 180  
Db 121 TCGCGCTTCGGGCGCAGCGGCTGCTGAGGCTGTCGAGAGTACGACGCGGCGGCGGCGGCGG 180  
QY 181 TACTTCTTCGACCGGCACTCGGAGGCTTCGGGCTTCATCTGCTTACGTCGCGGCGGCGG 240  
Db 181 TACTTCTTCGACCGGCACTCGGAGGCTTCGGGCTTCATCTGCTTACGTCGCGGCGGCGG 240  
QY 241 GCGAGCTGCGTTCGCGCGCGGAGTGTGCGAGTCTCTCTTACAAAGAGATGATCTAC 300  
Db 241 GCGAGCTGCGTTCGCGCGCGGAGTGTGCGAGTCTCTCTTACAAAGAGATGATCTAC 300  
QY 301 TGGGGCTTCGAGGCGCGCACTTCGAGTACTGCTGCGAGCGGCGGCTTCGACGCGGCGG 360  
Db 301 TGGGGCTTCGAGGCGCGCACTTCGAGTACTGCTGCGAGCGGCGGCTTCGACGCGGCGG 360  
QY 361 TCCGACACCTACACCTTCTACTCGCGCGGAGCGGCGGCTGCGGCGGCGGCGGCGGCGG 420  
Db 361 TCCGACACCTACACCTTCTACTCGCGCGGAGCGGCGGCTGCGGCGGCGGCGGCGGCGG 420  
QY 421 CGCCCGCGGCGGCGGCGGCGGCTCCCTCCAGCGGCTGCGTGGAGCGGCTGCGGCGGCGG 480  
Db 421 CGCCCGCGGCGGCGGCGGCGGCTCCCTCCAGCGGCTGCGTGGAGCGGCTGCGGCGGCGG 480  
QY 481 TTCGAGAGCCCACTGCTGCTGCGCGGCGGAGATCTGCGCTAGCTGCTGCGGCTGCTGTC 540  
Db 481 TTCGAGAGCCCACTGCTGCTGCGCGGCGGAGATCTGCGCTAGCTGCTGCGGCTGCTGTC 540  
QY 541 GTATCGTGTCCATGTTGTTGCTGTGCGCGGCGGAGCACTGCGGCGGCGGCGGCGGCGG 600  
Db 541 GTATCGTGTCCATGTTGTTGCTGTGCGCGGCGGAGCACTGCGGCGGCGGCGGCGGCGG 600

QY 601 GCCGACAAACCGCAGCCTGGATGACCGGAGCAGGATAATGAAGCTATCTGCATAGTTGG 660  
Db 601 GCCGACAAACCGCAGCCTGGATGACCGGAGCAGGATAATGAAGCTATCTGCATAGTTGG 660  
QY 661 TTCACTGCCAGTGCATCGTGGAGTTTCATTTCTCCAAAACCAAGTGTGAGTTTGTCAAG 720  
Db 661 TTCACTGCCAGTGCATCGTGGAGTTTCATTTCTCCAAAACCAAGTGTGAGTTTGTCAAG 720  
QY 721 AGACCCCTGAACATCATTTTACTTGGCAATCAACCGCGTATTACATCTCTGTGTTGATG 780  
Db 721 AGACCCCTGAACATCATTTTACTTGGCAATCAACCGCGTATTACATCTCTGTGTTGATG 780  
QY 781 ACAGTGTTCACGGCGAGAACTCTCACTCCAGGGGCTGGAGTCACTTGGAGG 834  
Db 781 ACAGTGTTCACGGCGAGAACTCTCACTCCAGGGGCTGGAGTCACTTGGAGG 834  
RESULT 8  
US-10-415-378-39  
; Sequence 39, Application US/10415378  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom  
; APPLICANT: YUE, Henry; NGUYEN, Dannel B.;  
; APPLICANT: HAPALIA, April J.A.; ELLIOTT, Vicki S.;  
; APPLICANT: LU, Yan; CHAWLA, Narinder K.;  
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;  
; APPLICANT: GANDHI, Ameena R.; DING, Li;  
; APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;  
; APPLICANT: ARVIZU, Chandra S.; GIEZEN, Kimberly J.;  
; APPLICANT: LAU, Preeti G.; AZIMZAI, Yalda;  
; APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;  
; APPLICANT: THORNTON, Michael B.; LU, Dying Aina M.;  
; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;  
; APPLICANT: ISON, H. Craig; DAS, Debopriya;  
; APPLICANT: RAMMANN, Brigitte E.; POLICKY, Jennifer L.;  
; APPLICANT: KEARNEY, Liam  
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS  
; FILE REFERENCE: PI-0270 USN  
; CURRENT APPLICATION NUMBER: US/10/415,378  
; CURRENT FILING DATE: 2003-05-07  
; PRIOR APPLICATION NUMBER: PCT/US01/46055  
; PRIOR FILING DATE: 2001-10-27  
; PRIOR APPLICATION NUMBER: US 60/250,790  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/252,232  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/249,661  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/247,673  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/245,904  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/243,989  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PERL Program  
; SEQ ID NO 39  
; LENGTH: 2235  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7482060CB1  
US-10-415-378-39  
Query Match 57.0%; Score 729; DB 51; Length 2235;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 514 ATCTCTGGCTAGCGTGTGCGTGGTGTGCTGATCGTGTCCATGCTGCTGCGCCAGC 573  
Db 920 ATCTCTGGCTAGCGTGTGCGTGGTGTGCTGATCGTGTCCATGCTGCTGCGCCAGC 979



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RESULT 11
PCT-US03-33087-85
; Sequence 85, Application PC/TUS0333087
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; Hafalia, April J.A.;
; APPLICANT: KEARE, Reena; LAL, Preeti G.;
; APPLICANT: YUE, Henry; BAUGHN, Mariiah R.;
; APPLICANT: THORNTON, Michael B.; LU, Dying Aina M.;
; APPLICANT: ISON, Craig H.; BECHA, Shanya D.;
; APPLICANT: DING, Li; WARREN, Bridget A.;
; APPLICANT: LEE, Soo Yeun; SWARNAKAR, Anita;
; APPLICANT: ELLIOTT, Vicki S.; RICHARDSON, Thomas W.;
; APPLICANT: MARQUIS, Joseph P.; RAMKUMAR, Jayalaxmi;
; APPLICANT: MURAGE, Jaji; RAUMANN, Brigitte E.;
; APPLICANT: YAO, Monique G.; LU, Yan;
; APPLICANT: GIETZEN, Kimberly J.; YANG, Yonghong G.;
; APPLICANT: CHANG, Hsin-Ru; CHAWLA, Narinder K.;
; APPLICANT: TRAN, Uyen K.; LEE, Sally;
; APPLICANT: YANG, Junming; GANDHI, Ameena R.;
; APPLICANT: TRIBULESY, Catherine M.; POLICKY, Jennifer L.;
; APPLICANT: RING, Huijun Z.; LEE, Ernestine A.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-1591 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/33087
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 60/419,313
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/421,033
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/421,349
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/423,516
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PERL Program
; SEQ ID NO 85
; LENGTH: 2204
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7523683CB1
PCT-US03-33087-85

Query Match          50.6%; Score 647; DB 1; Length 2204;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      632 GGATAATTGAAGCTATCTGTCATAGGTGGTTCACTGCCGAGTGCATCGTGAGGTTTCATTG 691
Db      1091 GGATAATTGAAGCTATCTGTCATAGGTGGTTCACTGCCGAGTGCATCGTGAGGTTTCATTG 1150
Qy      692 TCTCCAAAAACAAGTGTGAGTTTGTCAAGAGA CCCCTGAACCATCATTTGATTTACTGGCAA 751
Db      1151 TCTCCAAAAACAAGTGTGAGTTTGTCAAGAGA CCCCTGAACCATCATTTGATTTACTGGCAA 1210
Qy      752 TCAGCCGGTATTACATCTCTGCTTCATGATGACAGTGTTTACAGCGGAGAACTCTCAACTCC 811
Db      1211 TCAGCCGGTATTACATCTCTGCTTCATGATGACAGTGTTTACAGCGGAGAACTCTCAACTCC 1270
Qy      812 AGAGGGCTGGAGTCACTCCTTGAGGGGTACTTAGAATGATGAGGATTTTTTGGTGATTAAGC 871
Db      1271 AGAGGGCTGGAGTCACTCCTTGAGGGGTACTTAGAATGATGAGGATTTTTTGGTGATTAAGC 1330
Qy      872 TTGCCCGTCATCTTCATTGGTCTTCAGACACTCGTTTGACTCTCAACACGTTGCTACCAG 931
Db      1331 TTGCCCGTCATCTTCATTGGTCTTCAGACACTCGTTTGACTCTCAACACGTTGCTACCAG 1390
Qy      932 AGATGGTTATGTTACTTGTCTTCATTGTGTGTGCCATGGCAATCTTTTAGTGCATTTTCTC 991
Db      1391 AGATGGTTATGTTACTTGTCTTCATTGTGTGTGCCATGGCAATCTTTTAGTGCATTTTCTC 1450
Qy      992 AGCTTCTTGAAACATGGGCTGGAGCTGGAAACATCCAAAGGACTTTTACAGCAATTCCTG 1051

```



```
/ APPLICANT: Malyankar, Uriel M.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Liu, Ziaohong
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Li, Li
/ APPLICANT: Vernet, Corine
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Gorman, Linda
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Padigaru, Muralichara
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Gangolli, Esha A.
/ APPLICANT: Taupier Jr., Raymond J.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Anderson, David W.
/ APPLICANT: Liette, Mario W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Stone, David J.
/ APPLICANT: MacDougall, John R.
/ APPLICANT: Rothenberg, Mark E.
/ TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-322C
/ CURRENT APPLICATION NUMBER: US/10/114,270
/ PRIOR FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/281,086
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,020
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/282,930
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,512
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 470
/ SEQ ID NO 45
/ LENGTH: 1651
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1642)
US-10-114-270-45

Query Match      48.0%; Score 613; DB 45; Length 1651;
Best Local Similarity 100.0%; Pred. No. 1.6e-309;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      630  CAGGATAAATGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCAT 689
Db      792  CAGGATAAATGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCAT 851
QY      690  TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTTACTGGC 749
Db      852  TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTTACTGGC 911
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QY      750  AATCAGCCCGCTATTACATCTCTGTGTATGATGACAGTGTTTACAGGCGAGAACTCTCAACT 809
Db      912  AATCAGCCCGCTATTACATCTCTGTGTATGATGACAGTGTTTACAGGCGAGAACTCTCAACT 971
QY      810  CCAGAGGGCTGGAGTCAACCTTGAGGGTACTTAAATGATGAGGATTTTTTGGGTGATTAA 869
Db      972  CCAGAGGGCTGGAGTCAACCTTGAGGGTACTTAAATGATGAGGATTTTTTGGGTGATTAA 1031
QY      870  GCTTGCCTGTCACCTTCACTTGGTCTTTCAGACACATCGGTTTGACTCTCAACGTTGCTACCG 929
Db      1032  GCTTGCCTGTCACCTTCACTTGGTCTTTCAGACACATCGGTTTGACTCTCAACGTTGCTACCG 1091
QY      930  AGAGATGGTTATGTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 989
Db      1092  AGAGATGGTTATGTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1151
QY      990  TCAGCTTCTTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGACTTTTACCAGCAATCC 1049
Db      1152  TCAGCTTCTTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGACTTTTACCAGCAATCC 1211
QY      1050  TGTGCTGCTGCTGGTGGTGAATATCTATGACTACAGTTGGCTATGGAGATATGTATCC 1109
Db      1212  TGTGCTGCTGCTGGTGGTGAATATCTATGACTACAGTTGGCTATGGAGATATGTATCC 1271
QY      1110  TATCACAGTGCCTGGAAGAAATTTCTTGAGGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1169
Db      1272  TATCACAGTGCCTGGAAGAAATTTCTTGAGGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1331
QY      1170  GGCATTAACCTATACATTTTATCTACCATAGCTTTGTCAGTGTGTATCATGAGCTCAAGTT 1229
Db      1332  GGCATTAACCTATACATTTTATCTACCATAGCTTTGTCAGTGTGTATCATGAGCTCAAGTT 1391
QY      1230  TAGATCTGCTAGG 1242
Db      1392  TAGATCTGCTAGG 1404
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## RESULT 14

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PCT-US02-23407-26
; Sequence 26, Application PC/TUS0223407
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB-
; TITLE OF INVENTION: K-alpha2
; FILE REFERENCE: D0161 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/23407
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-23407-26
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Query Match      46.5%; Score 594; DB 1; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.5e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      634  ATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCATTTGC 693
Db      1  ATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCATTTGC 60
QY      694  TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTTACTGGCAATC 753
Db      61  TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTTACTGGCAATC 120
QY      754  ACGCGGTATTAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 813
Db      121  ACGCGGTATTAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
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QY 459 GCTGAGCGCATGCGCGGACCTTCGAGGAGCCACGTCGCTGCTGCGCGCGAGATCCT 518
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Db 61  GCTGAGCGCATGCGCGGACCTTCGAGGAGCCACGTCGCTGCTGCGCGCGAGATCCT 120
    |||
QY 519 GCTGAGCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
    |||
Db 121 GCTGAGCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
    |||
QY 579 GCTGAGCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 638
    |||
Db 181 GCTGAGCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
    |||
QY 639 TGAAGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
    |||
Db 241 TGAAGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    |||
QY 699 AAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGCAATACAGCC 758
    |||
Db 301 AAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGCAATACAGCC 360
    |||
QY 759 GTATTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
    |||
Db 361 GTATTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
    |||
QY 819 TGGAGTCACCTTGAGG 834
    |||
Db 421 TGGAGTCACCTTGAGG 436
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```

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RESULT 5
US-60-545-213-26268
; Sequence 26268, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26268
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26268

```

```

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 CCGAGAGATGTTTATGTTTACTTCTC 951
Db 1 CCGAGAGATGTTTATGTTTACTTCTC 25

```

```

RESULT 6
US-60-545-213-26269
; Sequence 26269, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26269
; TYPE: DNA

```

```

; ORGANISM: probe
US-60-545-213-26269
Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 928 CGAGAGATGTTTATGTTTACTTCTC 952
Db 1 CGAGAGATGTTTATGTTTACTTCTC 25

RESULT 7
US-60-545-213-26270
; Sequence 26270, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26270
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26270

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```

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 GAGATGTTTATGTTTACTTCTC 955
Db 1 GAGATGTTTATGTTTACTTCTC 25

```

```

RESULT 8
US-60-545-213-26271
; Sequence 26271, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26271
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26271

```

```

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 AGAGATGTTTATGTTTACTTCTC 954
Db 1 AGAGATGTTTATGTTTACTTCTC 25

```

```

RESULT 9
US-60-545-213-26272
; Sequence 26272, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth

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; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26272
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26272

Query Match      2.0%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 929 GAGAGATGGTTATGTTACTTCTT 953
Db 1 GAGAGATGGTTATGTTACTTCTT 25

RESULT 10
US-60-545-213-26273
; Sequence 26273, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26273
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26273

Query Match      2.0%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 932 AGATGGTTATGTTACTTCTTCA 956
Db 1 AGATGGTTATGTTACTTCTTCA 25

RESULT 11
US-60-545-213-26274
; Sequence 26274, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26274
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26274

Query Match      2.0%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 GATGGTTATGTTACTTCTTCA 957
Db 1 GATGGTTATGTTACTTCTTCA 25

RESULT 12
US-60-545-213-26275
; Sequence 26275, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26275
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26275

Query Match      2.0%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 CTACCGAGATGGTTATGTTACTT 948
Db 1 CTACCGAGATGGTTATGTTACTT 25

RESULT 13
US-60-545-213-26276
; Sequence 26276, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26276
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26276

Query Match      2.0%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 925 TACCGAGATGGTTATGTTACTT 949
Db 1 TACCGAGATGGTTATGTTACTT 25

RESULT 14
US-60-545-213-26277
; Sequence 26277, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
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; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26277  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-60-545-213-26277

Query Match 2.0%; Score 25; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 TGTACTTGTCTTCATTTGTGTTC 965  
Db 1 TGTACTTGTCTTCATTTGTGTTC 25

RESULT 15  
US-60-545-213-26278  
; Sequence 26278, Application US/60545213  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042099)  
; CURRENT APPLICATION NUMBER: US/60/545,213  
; CURRENT FILING DATE: 2004-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26278  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-60-545-213-26278

Query Match 2.0%; Score 25; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 TTGCTACCGAGAGATCGTTATGTTA 945  
Db 1 TTGCTACCGAGAGATCGTTATGTTA 25

Search completed: April 19, 2004, 20:55:14  
Job time : 149 secs

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 16:21:11 ; Search time 5112 seconds  
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Title: US-10-016-647-1  
Perfect score: 1278  
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Searched: 3470272 seqs, 21671516995 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 2: gb.htg.\*
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- 7: gb.ph.\*
- 8: gb.pl.\*
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- 12: gb.sv.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
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- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
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- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pin.\*
- 35: em.htg.rod.\*
- 36: em.htg.man.\*
- 37: em.htg.vrt.\*
- 38: em.sv.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1278	100.0	1278	6	AX511260	Sequence
2	1278	100.0	1844	6	AX511262	Sequence
3	1278	100.0	3670	9	AF454547	Homo sapi
4	1235	96.6	1311	9	AB070604	Homo sapi
5	1235	96.6	1947	6	AX641934	Sequence
6	1235	96.6	1947	9	AF348982	Homo sapi
7	1235	96.6	3703	9	AF454548	Homo sapi
8	1178.4	92.2	2235	6	AX478109	Sequence
9	1115.6	87.3	3323	10	AF454551	Mus muscu
10	1099.6	86.0	1744	10	AF454549	Rattus no
11	1072.6	83.9	3356	10	AF454552	Mus muscu
12	1070	83.7	5775	6	AX641960	Sequence
13	1056.6	82.7	1302	9	AF450110	Homo sapi
14	1056.6	82.7	1777	10	AF454550	Rattus no
15	846.6	66.2	2312	6	AX392945	Sequence
16	805.4	63.0	1038	10	AB070605	Rattus no
17	649	50.8	151367	9	AC025750	Homo sapi
18	577	45.1	209523	10	AC084366	Mus muscu
19	553	43.3	219807	2	AC098764	Rattus no
20	553	43.3	259704	2	AC112092	Rattus no
21	553	43.3	268099	2	AC133407	Rattus no
22	383	30.0	461	6	AX319980	Sequence
23	377.8	29.6	68831	2	AC101224	Mus muscu
24	348.4	27.3	777	6	AX534980	Sequence
25	336.4	26.3	911	6	AX534981	Sequence
26	283.8	22.2	1401	9	HSA011021	Homo sapi
27	278.8	21.8	3348	10	RSRKLIPC	X16476 Rat drk1 ge
28	278.4	21.8	2203	9	BC045629	Homo sapi
29	277.4	21.7	1542	9	AF033383	Homo sapi
30	277.4	21.7	2127	6	T81198	Sequence 1
31	277.4	21.7	2127	6	BD14650	Potassium
32	264.4	20.7	2574	10	MUSSHAB	M64228 Mouse potas
33	264.4	20.7	2707	10	BC051422	Mus muscu
34	264.4	20.7	3525	10	BC031776	Mus muscu
35	264.4	20.7	3733	10	BC061501	Mus muscu
36	262	20.5	1560	6	AX641932	Sequence
37	262	20.5	1560	9	AF348984	Homo sapi
38	262	20.5	1560	9	AF450108	Homo sapi
39	260.6	20.4	2577	9	AF026005	Homo sapi
40	260.6	20.4	3054	9	HSDRK1	X68302 H.sapiens h
41	260.4	20.4	2523	10	RRA011020	Rattus ra
42	260.2	20.4	3777	6	AX641938	Sequence
43	260.2	20.4	3777	9	HUMKV21CH	L02840 Homo sapien
44	258.8	20.3	2022	6	BD235203	Voltage g
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ALIGNMENTS

RESULT 1	AX511260	AX511260	1278 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	Sequence 1 from Patent WO0250271.					
DEFINITION	Sequence 1 from Patent WO0250271.					
ACCESSION	AX511260					
VERSION	AX511260.1	GI:23392138				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1					
AUTHORS	Friddle,C.J., Hilbun,E. and Turner,C.A.					
TITLE	Novel human ion channel protein and polynucleotides encoding the same					

Pred. No. is the number of results predicted by chance to have a



JOURNAL Patent: WO 0250271-A 1 27-JUN-2002;  
 Lexicon Genetics Incorporated (US)  
 Location/Qualifiers  
 FEATURES  
 source  
 1..1278  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1278; DB 6; Length 1278;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-170;  
 Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACCTTCGGGCGCAGCGGGGGGCTCGTGGTGTGAACTGGGCGGCGCGCGTAT 60  
 Db 1 ATGACCTTCGGGCGCAGCGGGGGGCTCGTGGTGTGAACTGGGCGGCGCGCGTAT 60

Qy 61 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGCTGCGCGCGTGAAGCGGCTGCAACGGC 120  
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Qy 121 TGGCGTCCGAGCGCGAGCTGCTGAGGCTGCGAGCTACGACCGCGAGCGCAACGAG 180  
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Qy 181 TACTTCTTCGACCGGCACTCGGAGGCTTCCGGCTTCACTGCTCTACGTCGCGGCCAC 240  
 Db 181 TACTTCTTCGACCGGCACTCGGAGGCTTCCGGCTTCACTGCTCTACGTCGCGGCCAC 240

Qy 241 GGCAAGTGGCTTCGCGCGCGGATGTGAGCTCTCTCTTACAAAGAGATGATCTAC 300  
 Db 241 GGCAAGTGGCTTCGCGCGCGGATGTGAGCTCTCTCTTACAAAGAGATGATCTAC 300

Qy 301 TGGGGCTGAGCGCGGCGACTCGAGTACTGTCGAGCGGCGGCTCGACGCGCGATG 360  
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Qy 361 TCGGACACCTTACACCTTCTACTCGGCGGAGCGAGCGGCGGCTGCGCGCGGCGGCG 420  
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Qy 421 CGCGCGCGCGCGCGGCGGCTTCTCTAGCGGCTGCTGAGCGGCTGCGCGGCGGCG 480  
 Db 421 CGCGCGCGCGCGCGGCGGCTTCTCTAGCGGCTGCTGAGCGGCTGCGCGGCGGCG 480

Qy 481 TTGAGGAGCGGCGGCGGCTGCTGAGCGGCTGCTGAGCGGCTGCTGAGCGGCTGCTG 540  
 Db 481 TTGAGGAGCGGCGGCGGCTGCTGAGCGGCTGCTGAGCGGCTGCTGAGCGGCTGCTG 540

Qy 541 GTGATCGTGTCCATGCTGCTGCGCGGCGGCTGCTGAGCGGCTGCTGAGCGGCTGCT 600  
 Db 541 GTGATCGTGTCCATGCTGCTGCGCGGCGGCTGCTGAGCGGCTGCTGAGCGGCTGCT 600

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Qy 721 AGACCCCTGACATCATGTTACTGGAATCAAGCGGCTTACATCTCTGTTGATG 780  
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Qy 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCGGCTCACTTATGTTGCTTCAGACA 900  
 Db 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCGGCTCACTTATGTTGCTTCAGACA 900

Qy 901 CTCGGTTGACTCTCAACCGTTGCTACCGAGAGATGGTTACTGTCTTCACTTGT 960  
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Qy 961 GTTCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAAACATGGCTGGACCTGAA 1020  
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Qy 1021 ACATCCAAACAGGACTTTTACCAGCAATTCCTGCTGCTGCTGGTGGGTGATTATCTCTATG 1080  
 Db 1021 ACATCCAAACAGGACTTTTACCAGCAATTCCTGCTGCTGCTGGTGGGTGATTATCTCTATG 1080

Qy 1081 ACTACAGTTGGCTATGAGATATGATCTTATCAGTGCCTGGAAGAACTCTGGAGGA 1140  
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Qy 1201 TTTGTGAGTGTATCATGAGCTCAAGTTTATAGATCTGCTAGGTATAGTAGAGCTCTCC 1260  
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Qy 1261 ACTCAATTCCTGAATTA 1278  
 Db 1261 ACTCAATTCCTGAATTA 1278

RESULT 2

AX511262 1844 bp DNA linear PAT 27-SEP-2002  
 DEFINITION Sequence 3 from Patent WO0250271.  
 ACCESSION AX511262  
 VERSION AX511262.1 GI:23392139  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Fridde, C.J., Hilbun, E. and Turner, C.A.  
 TITLE Novel human ion channel protein and polynucleotides encoding the same  
 JOURNAL Patent: WO 0250271-A 3 27-JUN-2002;  
 Lexicon Genetics Incorporated (US)  
 FEATURES  
 source  
 1..1844  
 /organism="Homo sapiens"  
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ORIGIN

Query Match 100.0%; Score 1278; DB 6; Length 1844;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-170;  
 Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGCTGCGCGCGTGAAGCGGCTGCAACGGC 120  
 Db 517 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGCTGCGCGCGTGAAGCGGCTGCAACGGC 576

Qy 121 TGGCGTCCGAGCGGAGCTGCTGAGGCTGCGAGCTTACGACCGCGAGCGCAACGAG 180  
 Db 577 TGGCGTCCGAGCGGAGCTGCTGAGGCTGCGAGCTTACGACCGCGAGCGCAACGAG 636

Qy 181 TACTTCTTCGACCGGCACTCGGAGGCTTCCGGCTTCACTGCTCTACGTCGCGGCCAC 240  
 Db 637 TACTTCTTCGACCGGCACTCGGAGGCTTCCGGCTTCACTGCTCTACGTCGCGGCCAC 696

241 GGCAGAGCTGCGCTTCGCGCGGATGCGAGCTCTCTTCTCAACAGAGATGATCTAC 300  
Db |||||  
697 GGCAGAGCTGCGCTTCGCGCGGATGCGAGCTCTCTTCTCAACAGAGATGATCTAC 756  
Qy |||||  
301 TGGGGCTGGAGGGCGCGACCTCGAGTACTCTCTCCAGCGCGCTCTCGACGCGCATG 360  
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361 TCGGACACTACACTTCTACTCCGCGCAGCAGCGCGCTCTGGCGCGGAGGAGCG 420  
Db |||||  
817 TCGGACACTACACTTCTACTCCGCGCAGCAGCGCGCTCTGGCGCGGAGGAGCG 876  
Qy |||||  
421 CGCCCGCGCGCGCGCGCGCTCCCTCCAGCGCGCTCTGGAGCGCATCGCGGAGCC 480  
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Qy |||||  
481 TTCGAGGAGCCCACTGCTGCTGCGCGCGCAGATCTCTGGCTAGCGTCTCGTGTGTC 540  
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781 ACAGTGTTCAGGCGAGACTCTCACTCAGAGGCTGGAGTCACTTGGAGTACTT 840  
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901 CTCGGTTTGAATCTCAAGCTTCTACCGAGAGATGTTATGTTATCTTCTTCAATTTGT 960  
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961 GTTGCCATGCAATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGGCTGACCTGAA 1020  
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1417 GTTGCCATGCAATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGGCTGACCTGAA 1476  
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Db |||||  
1717 ACTGAATTCCTGAATTA 1734

RESULT 3  
LOCUS AF454547 3670 bp mRNA linear PRI 09-AUG-2002  
DEFINITION Homo sapiens voltage-gated potassium channel subunit Kv10.1a mRNA, complete cds, alternatively spliced.  
ACCESSION AF454547  
VERSION AF454547.1 GI:22164081  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3670)  
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.  
TITLE Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3670)  
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA  
FEATURES  
Location/Qualifiers  
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GWFAECIVRFIVSKNCFKRPPLNIIIDLLATIPYIIVLMVTFTGNSQLQAGVT  
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polyA\_site 3670  
ORIGIN  
Query Match 100.0%; Score 1278; DB 9; Length 3670;  
Best Local Similarity 100.0%; Pred. No. 6.9e-170;  
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGACCTTCGGCGCAGCGCGCGCTCGGTGCTGCTGACGTGGCGCGCGCGGTAT 60  
Db 478 ATGACCTTCGGCGCAGCGCGCGCTCGGTGCTGCTGACGTGGCGCGCGCGGTAT 537  
Qy 61 TCGCTGTCCCGGAGCTGCTGAAGACTTTCCTGCTGCGCGCGCTGAGCGCGCTCACGGC 120  
Db 538 TCGCTGTCCCGGAGCTGCTGAAGACTTTCCTGCTGCGCGCGCTGAGCGCGCTCACGGC 597  
Qy 121 TCGCGCTCCGAGCGCAGCTGCTCGAGGTGTCGAGACTACGACCGGAGCGCAACGAG 180  
Db 598 TCGCGCTCCGAGCGCAGCTGCTCGAGGTGTCGAGACTACGACCGGAGCGCAACGAG 657  
Qy 181 TACTTCTTCGACCGCACTCGAGGCTTCCTGCTTCTCTGCTCTAGCTCGCGCGCCAC 240  
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778 TGGGGCTGGAGGCGGCGCCTCGAGTACTGTGCGAGCGCGCTCGACGACCGCATG 837  
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 838 TCCGACACCTACACTTCTACTCGGCGCGAGCGCGGCGTGTGGCGCGGACGAGGG 897  
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 1138 TTCACTCGGAGTGCATGCTGAGGTTCAATGTTCTCAAAAACAAGTGTGAGTTTCAAG 1197  
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 1198 AGACCCCTGAACATCATGATTTACTGGGAAATCAGCGCGTATTACATCTCTGTGTTGATG 1257  
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 1261 ACTGAATTCCTGAATTA 1278  
 1738 ACTGAATTCCTGAATTA 1755

RESULT 4  
 AB070604  
 LOCUS  
 DEFINITION  
 Homo sapiens KV6.3 mRNA for voltage-gated K+ channel 6.3, complete cds.  
 1311 bp mRNA linear PRI 23-MAR-2002

AB070604  
 AB070604.1 GI:18916472  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Sano, Y., Mochizuki, S., Miyake, A., Kitada, C., Inamura, K., Yokoi, H.,  
 Nozawa, K., Matsushima, H. and Furuichi, K.  
 Molecular cloning and characterization of Kv6.3, a novel modulatory  
 subunit for voltage-gated K+ channel Kv2.1  
 FEBS Lett. 513, 230-234 (2002)  
 2 (bases 1 to 1311)  
 Direct Submission  
 Sano, Y. and Mochizuki, S.  
 Submitted (24-AUG-2001) Yoritaka Sano, Yamanouchi Pharmaceutical  
 Co., Ltd, Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba,  
 Ibaraki 305-8585, Japan (E-mail: sano.yorikata@yamanouchi.co.jp,  
 Tel:81-298-52-5111, Fax:81-298-52-2965)  
 Location/Qualifiers  
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Query Match 95.6%; Score 1235; DB 9; Length 1311;  
 Best Local Similarity 97.5%; Pred. No. 8.2e-164;  
 Matches 1278; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
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 Snyders,D.J., Ottschyttsch,N., Raes,A. and van Hoorick,D.  
 New heterotetrameric potassium channels and uses thereof  
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VERSION			
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SOURCE			
ORGANISM			
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REFERENCE			
1 (bases 1 to 1947)			
Ottschytsh, N., Raes, A., Van Hoorick, D. and Snyder, D.J.			
Obligatory heterotetramerization of three previously			
uncharacterized Kv channel alpha-subunits identified in the human			
genome			
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 7986-7991 (2002)			
JOURNAL			
MEDLINE			
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2 (bases 1 to 1947)			
Ottschytsh, N., van Hoorick, D., Raes, A.L. and Snyder, D.J.			
Direct Submission			
TITLE			
Submitted (14-PEB-2001) Molecular Biophysics, VIB (Flanders Inst.			
Biotechnology & University of Antwerp, Universiteitsplein 1,			
Antwerp 2610, Belgium			

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VERSION 1  
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REFERENCE 1 (bases 1 to 3703)  
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.  
TITLE Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium  
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JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3703)  
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-2001) Physiology and Neuroscience, New York  
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 REFERENCE 1  
 AUTHORS Tang, Y.T., Yue, H., Nguyen, D.B., Hafalia, A.J., Elliott, V.S., Lu, Y.,  
 Walla, N.K., Yao, M.G., Baughn, M.R., Gandhi, A.R., Ding, L.,  
 Sanjanwala, M., Ramkumar, J., Arvizu, C., Gietzen, K.J., Lal, P.G.,  
 Azimzai, Y., Khan, F.A., Thangavelu, K., Thornton, M., Lu, D.A.,  
 Tribouley, C.M., Warren, B.A., Ison, C.H., Das, D., Raumann, B.E.,  
 Policky, J.L. and Kearney, L.  
 TITLE Transporters and ion channels  
 JOURNAL Patent: WO 0240541-A 39 23-MAY-2002;  
 Incyte Genomics, Inc. (US)  
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LOCUS Mus musculus voltage-gated potassium channel subunit Kv10.1a mRNA,  
DEFINITION complete cds, alternatively spliced.  
ACCESSION AF454551  
VERSION AF454551.1 GI:22164089  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3323)  
Vega-Saenz de Miera, B.C. and Rudy, B.  
Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium  
channel subunits  
Unpublished  
2 (bases 1 to 3323)  
Vega-Saenz de Miera, B.C. and Rudy, B.  
Direct Submission  
TITLE Submitted (04-DEC-2001) Physiology and Neuroscience, New York  
JOURNAL University School of Medicine, 550 First Avenue, New York, NY  
10016, USA

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KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3356)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Vega-Saenz de Miera, E.C. and Rudy, B.  
Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits  
Unpublished

JOURNAL 2 (bases 1 to 3356)  
Vega-Saenz de Miera, E.C. and Rudy, B.  
Direct Submission  
Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA

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Location/Qualifiers

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VERSION			
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1 (bases 1 to 1302)			
AUTHORS			
Preisig-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.			
TITLE			
Cloning and characterization of two novel gamma Kv subunits			
JOURNAL			
Unpublished			
REFERENCE			
2 (bases 1 to 1302)			
AUTHORS			
Preisig-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.			
TITLE			
Direct Submission			
JOURNAL			
Submitted (23-NOV-2001) University of Marburg, Institute of Physiology, Deutschhausstrasse 1-2, Marburg 35037, Germany			
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Matches 1175; Conservative 0; Mismatches 94; Indels 42; Gaps 2;	
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QY	481 TTCGAGAGCGCACGTCGTCGTCGCGCGCGAGATCTGCTGAGGTGTCGCTGTCGTCG 540
Db	472 TTCGAGAGCGCACGTCGTCGTCGCGCGCGAGATCTGCTGAGGTGTCGCTGTCGTCG 531
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QY	601 GCGCAACCGCGAGCTGCGATGACCGGAGCA----- 631
Db	592 GCGCAACCGCGAGCTGCGATGACCGGAGCAGGTACTCCGCGCGCGCTGGGAGGAGCGCC 651
QY	632 ----GGATAATGAGCTATCTGATAGTGGTTCACCTCGCGAGTGCATCGTGGTTC 687
Db	652 TCGGAGATAATGAGCTATCTGATAGTGGTTCACCGCGAGTGCATCGTGGTTC 711
QY	688 ATTGTCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACATCATTTACTG 747
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Db	832 CTCGAGAGGCTGAGTCACTTCAGGCTTCTGAGTATGATGAGGATTTTGGGTGATT 891
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Db	892 AAGCTTCGCGCGCACTTCATCGCGCTTCAGACACTCGGTTGACTCTCAACGATGCTAC 951
QY	928 CGAGAGATGGTATGATGCTGCTTCAATGCTTGGTGGCATGCGCATCTTTAGTGCATT 987
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QY	1108 CCTATCACAGCTCGTGAAGAAATCTTGGAGGAGTTGTGTGTCAGTGAATTTCTA 1167
Db	1132 CCTATCACAGCTCGTGAAGAAATCTTGGAGGAGTTGTGTGTCAGTGGATCGTTCTG 1191
QY	1168 TTGGCATTAACCTATCACTTTTATCTACATAGCTTTGTGCACTGTTATCATGAGCTCAAG 1227
Db	1192 TTGGCATTAACCTATCACTTTTATCTACATAGCTTTGTGCACTGTTATCATGAGCTCAAG 1251
QY	1228 TTTAGATCTGCTAGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
Db	1252 TTTAGATCTGCTAGTATAGTAGGAGCTCTCCGCTGAGTTCCTGAATTA 1302
RESULT 14	
AF454550	1777 bp mRNA linear ROD 09-AUG-2002
LOCUS	Rattus norvegicus voltage-gated potassium channel subunit Kv10.1b
DEFINITION	mRNA, complete cds, alternatively spliced.
ACCESSION	AF454550
VERSION	AF454550.1 GI:22164087
KEYWORDS	
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
REFERENCE	1 (bases 1 to 1777)
AUTHORS	Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE	Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1777)
AUTHORS	Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE	Direct Submission
JOURNAL	Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA
FEATURES	Location/Qualifiers
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Query Match	82.7%; Score 1056.6; DB 10; Length 1777;
Best Local Similarity	89.6%; Pred. No. 8e-139;
Matches 1175; Conservative	0; Mismatches 94; Indels 42; Gaps 2;
QY	1 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTCTGAACTGGGGCGGCGCCCGGTAT 60
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287 TCGCTGTCGGGAGCTGCTCAAGAACTTCCCGCTGCGCGCTGTGTCAGCCGCTGCACGGC 346  
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467 GCGAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTAC 526  
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AX392945  
LOCUS AX392945 2312 bp DNA linear PAT 23-MAR-2002  
DEFINITION Sequence 47 from Patent WO0212340.  
ACCESSION AX392945  
VERSION AX392945.1 GI:19700992  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Yue, H., Thornton, M., Ramkumar, J., Tang, Y.T., Azimzai, Y.,  
Baughn, M.R., Yang, J., Yao, M.G., Lal, P., Wallia, N.K., Gandhi, A.R.,  
Hafalia, A.J., Nguyen, D.B., Patterson, C., Elliott, V.S.,  
Tribouley, C.M., Lu, D.A., Xu, Y., Reddy, R., Hernandez, R.,  
Borowsky, M.L., Lo, T.P., Lu, Y., Policky, J.L., Greene, B.D.,  
Sanjanwalla, M.S., Raumann, B.E., Burford, N., Ison, C.H., Lee, E.A.,  
Ding, L., Das, D., Kallick, D.A., Khan, F.A. and Seilhamer, J.J.  
JOURNALS Patent: WO 0212340-A 47 14-FEB-2002;  
FEATURES Location/Qualifiers  
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Query Match 66.2%; Score 846.6; DB 6; Length 2312;  
Best Local Similarity 93.3%; Pred. No. 2.1e-109;  
Matches 885; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 330 CTGTGCGGCGCGCTTCGACGACCGCATGCTCGACACCTTCTACTCGGCGCA 389  
Db 897 CTGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGAGCTACGACCGGAGCGCAACGA 956  
QY 390 CGAGCGGCGTGTGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 449  
Db 957 GTACTTCTTCACCGCGCACTCGGAGGCTTTCGCGTTCATCTCTACGCGGCTCCTC 1016  
QY 450 CAGCGCTGCGTGGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTGCTGCGGCGCG 509  
Db 1017 CAGCGCTGCGTGGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTGCTGCGGCGCG 1076  
QY 510 CGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 569  
Db 1077 CGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1136  
QY 570 CAGCGCTGCGGCGCATGCGCGGACCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGG 629  
Db 1137 CAGCGCTGCGGCGCATGCGCGGACCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGG 1196  
QY 630 CAGGATAATTAAGCTATCTGCAATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 689  
Db 1197 CAGGATAATTAAGCTATCTGCAATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1256  
QY 690 TGTCTCCAAAACAACTGTGAGTGTGTTTGAAGTGTGTTTGAAGTGTGTTTGAAGTGTG 749  
Db 1257 TGTCTCCAAAACAACTGTGAGTGTGTTTGAAGTGTGTTTGAAGTGTGTTTGAAGTGTG 1316  
QY 750 AATCACGCGGTATTAATCTCTGTTGTTGATGACAGTGTGTTTACAGGCGGAGAACTCTCA 809  
Db 1317 AATCACGCGGTATTAATCTCTGTTGTTGATGACAGTGTGTTTACAGGCGGAGAACTCTCA 1376



QY	810	CCAGAGGCTGAGTACACCTTGAGGGTACTTAGAATGATGAGGATTTTGGGTGATTAA	869
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QY	1110	TATCAGAGTGCCTGGAGAAATCTTGGAGAGTTTGTGTGTCAGTGGAAATGTTCTATT	1169
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QY	1230	TAGATCTGCTAGGTATAGTAGAGGCTCTCCACTGAATTCCTGAAATTAA	1278
Db	1797	TAGATCTGCTAGGTATAGTAGAGGCTCTCCACTGAATTCCTGAAATTAA	1845

Search completed: October 6, 2004, 19:32:44  
Job time : 5127 secs



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 16:14:11 ; Search time 577 Seconds

(without alignments)

9409.354 Million cell updates/sec

Title: US-10-016-647-1

Perfect score: 1278  
Sequence: 1 atgacctcgggcgcgcgg.....ccactgaattcctgaattaa 1278

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 29Jan04: \*  
1: Geneseqn1980s: \*  
2: Geneseqn1990s: \*  
3: Geneseqn2000s: \*  
4: Geneseqn2001as: \*  
5: Geneseqn2001bs: \*  
6: Geneseqn2002s: \*  
7: Geneseqn2003as: \*  
8: Geneseqn2003bs: \*  
9: Geneseqn2003cs: \*  
10: Geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1278	100.0	1278	6 ABN83930	ABN83930 Human vol
2	1278	100.0	1844	6 ABN83931	ABN83931 Human vol
3	1235	96.6	1947	7 ABZ24711	ABZ24711 Human pot
4	1235	96.6	5174	9 ADD01447	Add01447 Human TCH
5	1232	96.4	1308	9 ADD01427	Add01427 Human TCH
6	1178.4	92.2	2235	6 ABX83228	ABX83228 Human tra
7	1099.4	86.0	1651	7 ABX72192	ABX72192 Human NOV
8	1070	83.7	5775	7 ABZ24716	ABZ24716 Murine po
9	846.6	65.2	2312	6 AD33662	Ad33662 Human TBI
10	729.8	57.1	950	9 ADD01469	Add01469 Mouse TCH
11	406.6	31.8	1634	6 ABQ49122	ABQ49122 Oligonuc1
12	406.6	31.8	1634	6 ABQ49123	ABQ49123 Oligonuc1
13	395.4	30.9	1634	6 ABQ49124	ABQ49124 Oligonuc1
14	395.4	30.9	1634	6 ABQ49125	ABQ49125 Oligonuc1
15	383	30.0	461	6 ABK27494	ABK27494 DNA encod
16	348.4	27.3	777	6 ABX91965	ABX91965 Lung, spec
17	336.4	26.3	911	6 ABX91966	ABX91966 Lung, spec
18	283.8	22.2	1401	2 AA223803	AA223803 Human Kv6
19	283.8	22.2	1401	5 AA575631	AA575631 DNA encod
20	280	21.9	2370	9 ADB47439	ADB47439 Human CDN
21	277.4	21.7	2127	2 AAT12461	AAT12461 Human K+
22	277.4	21.7	2127	2 AAV04873	AAV04873 cDNA sequ
23	277.4	21.7	2127	9 ADC99152	ADC99152 Human mat

24	262	20.5	1560	7 ABZ24710	ABZ24710 Human pot
25	260.6	20.4	2577	6 AAL45289	AAL45289 Human KCN
26	260.2	20.4	2565	3 AAZ36415	AAZ36415 cDNA enco
27	260.2	20.4	3777	7 ABZ24713	ABZ24713 Human pot
28	258.8	20.3	2022	3 AAZ49455	Aaz49455 Human vol
29	257.6	20.2	2499	6 ABZ35517	ABZ35517 Human gen
30	251	19.6	1518	3 AAZ49454	Aaz49454 Mouse Vol
31	226	17.7	3339	4 ABL01915	ABl01915 Drosophil
32	223.6	17.5	1446	2 AAZ23804	Aaz23804 Murine Kv
33	218.6	17.1	3441	4 ABL20763	ABl20763 Drosophil
34	201.4	15.8	1488	2 AAZ06653	Aaz06653 hkv5.1 hu
35	201.4	15.8	1880	2 AAZ06652	Aaz06652 hkv5.1 hu
36	198.2	15.5	1485	7 ABZ24715	ABZ24715 Human pot
37	198.2	15.5	2483	2 AAT12462	Aat12462 Human K+
38	198.2	15.5	2483	2 AAV04874	Aav04874 cDNA sequ
39	198.2	15.5	2483	9 ADC99154	Adc99154 Human mat
40	197.8	15.5	3102	2 AAZ11905	Aaz11905 Human pot
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42	171	13.4	998	4 AAI11882	AAi11882 Probe #18
43	171	13.4	998	4 ABA53583	ABa53583 Human foe
44	171	13.4	998	4 AAI33209	AAi33209 Probe #18
45	171	13.4	998	4 ABA43164	ABa43164 Human bre

## ALIGNMENTS

RESULT 1  
ABN83930  
ID ABN83930 standard; cDNA; 1278 BP.  
AC ABN83930;  
XX ABN83930;  
DT 06-SEP-2002 (first entry)  
XX Human voltage-gated potassium channel-like protein encoding cDNA.  
DE Human; voltage-gated potassium channel; ion channel; neuroprotective; therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;  
KW single nucleotide polymorphism; foetal brain; brain; cerebellum;  
KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;  
KW foetal liver; liver; testis; thyroid; salivary gland; stomach;  
KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;  
KW 12 week old embryo; adenocarcinoma; osteosarcoma; gene; ss.  
XX Homo sapiens.  
OS Homo sapiens.

FT Key Location/Qualifiers  
FT CDS 1..1278  
FT FT /\*tag= a  
FT FT /product= "voltage-gated potassium channel-like protein"  
FT FT replace(432,C)  
FT FT /\*tag= b  
FT FT /standard\_name= "single nucleotide polymorphism"  
XX WC200250271-A2.  
XX 27-JUN-2002.  
XX 10-DEC-2001; 2001WO-US048050.  
XX 20-DEC-2000; 2000US-0257932P.  
XX (LEXI-) LEXICON GENETICS INC.  
XX Fiddle CJ, Hilbun E, Turner CA;  
XX WPI; 2002-508799/54.  
XX P-PSDB; ABB83073.  
XX Human ion channel polynucleotide useful in therapeutic, diagnostic and pharmacogenomic applications.

Claim 1; Page 34; 36pp; English.

PS The invention relates to a novel human ion channel polynucleotide that  
 XX shares structural similarity with voltage-gated potassium channel  
 CC proteins. The activity of the protein of the invention may be described  
 CC as neuroprotective. The protein of the invention is useful in  
 CC therapeutic, diagnostic and pharmacogenomic applications, for example to  
 CC identify mutations associated with a particular disease, as a diagnostic  
 CC or prognostic assay, or in gene therapy. The protein of the invention has  
 CC been found to be expressed in human foetal brain, brain, cerebellum,  
 CC pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal  
 CC liver, liver, testis, thyroid, salivary gland, stomach, skeletal muscle,  
 CC heart, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo,  
 CC adenocarcinoma and osteosarcoma cells. The current sequence represents  
 CC the human voltage-gated potassium channel-like protein encoding CDNA  
 XX  
 XX

Sequence 1278 BP; 237 A; 349 C; 376 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 1278; DB 6; Length 1278;  
 Best Local Similarity 100.0%; Pred. No. 3e-260;  
 Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 721 AGACCCCTGAAATCATTTTACTGGCAATCAGCGCGTATTACATCTCTGTGTGTGT 780

QY 781 ACAGTGTTTACAGCGGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGAGTACTT 840  
 DB 781 ACAGTGTTTACAGCGGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGAGTACTT 840

QY 841 AGATGATGAGGATTTTGGGGTGAATTAAGCTTGGCGTCACTTCACTTGGTCTTCAGACA 900  
 DB 841 AGATGATGAGGATTTTGGGGTGAATTAAGCTTGGCGTCACTTCACTTGGTCTTCAGACA 900

QY 901 CTCGGTTTGACTCTCAAACTTCTACCGAGAGATGTTATCTGTCTTCACTTGT 960  
 DB 901 CTCGGTTTGACTCTCAAACTTCTACCGAGAGATGTTATCTGTCTTCACTTGT 960

QY 961 GTTCCGATGCAATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGCTGGACCTGGAA 1020  
 DB 961 GTTCCGATGCAATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGCTGGACCTGGAA 1020

QY 1021 ACATCCAAAGGACTTTTACAGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTATG 1080  
 DB 1021 ACATCCAAAGGACTTTTACAGCAATTCCTGCTGCTGCTGCTGCTGCTGCTATG 1080

QY 1081 ACTACAGTTGGCTATGAGATATGTTATCTTATGCGCATACCTATCTTATCTACCATAGC 1140  
 DB 1081 ACTACAGTTGGCTATGAGATATGTTATCTTATGCGCATACCTATCTTATCTACCATAGC 1140

QY 1141 GTTTGCTGTGCTAGTGAATTTTCTTATGCGCATACCTATCTTATCTTATCTACCATAGC 1200  
 DB 1141 GTTTGCTGTGCTAGTGAATTTTCTTATGCGCATACCTATCTTATCTTATCTACCATAGC 1200

QY 1201 TTTGTCAGTGTATCATGAGCTCAAGTTAGATCTGCTAGGTATAGTAGAGCCTCTCC 1260  
 DB 1201 TTTGTCAGTGTATCATGAGCTCAAGTTAGATCTGCTAGGTATAGTAGAGCCTCTCC 1260

QY 1261 ACTGAATTCCTGAATTA 1278  
 DB 1261 ACTGAATTCCTGAATTA 1278

RESULT 2  
 ASN83931  
 ID ASN83931 standard; DNA; 1844 BP.  
 XX  
 AC ASN83931;  
 XX  
 DT  
 XX  
 XX 06-SEP-2002 (first entry)  
 XX Human voltage-gated potassium channel-like protein encoding sequence.  
 DE Human; voltage-gated potassium channel; ion channel; neuroprotective;  
 XX therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;  
 KW single nucleotide polymorphism; foetal brain; brain; cerebellum;  
 KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;  
 KW foetal liver; liver; testis; thyroid; salivary gland; stomach;  
 KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;  
 KW 12 week old embryo; adenocarcinoma; osteosarcoma; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT 5'UTR 1..456  
 FT /\*tag= a  
 FT 457..1734  
 FT /\*tag= b  
 FT /product= "voltage-gated potassium channel-like protein"  
 FT /replace (888,C)  
 FT /\*tag= c  
 FT /standard\_name= "single nucleotide polymorphism"  
 FT 3'UTR 1735..1844  
 FT /\*tag= d  
 XX  
 XX WO200250271-A2.  
 XX 27-JUN-2002.  
 PD

XX 10-DEC-2001; 2001WO-US048050.  
 XX 20-DEC-2000; 2000US-0257932P.  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX Friddle CJ, Hilbun E, Turner CA;  
 XX WPI; 2002-508799/54.  
 XX P-PSDB; ABB83073.  
 XX Human ion channel polynucleotide useful in therapeutic, diagnostic and  
 XX pharmacogenomic applications.  
 XX Disclosure; Page 36; 36pp; English.  
 XX The invention relates to a novel human ion channel polynucleotide that  
 XX shares structural similarity with voltage-gated potassium channel  
 XX proteins. The activity of the protein of the invention may be described  
 XX as neuroprotective. The protein of the invention is useful in  
 XX therapeutic, diagnostic and pharmacogenomic applications, for example to  
 XX identify mutations associated with a particular disease, as a diagnostic  
 XX or prognostic assay, or in gene therapy. The protein of the invention has  
 XX been found to be expressed in human foetal brain, brain, cerebellum,  
 XX pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal  
 XX liver, liver, testis, thyroid, salivary gland, stomach, skeletal muscle,  
 XX heart, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo,  
 XX adenocarcinoma and osteosarcoma cells. The current sequence represents  
 XX the human voltage-gated potassium channel-like protein encoding DNA  
 XX sequence  
 XX Sequence 1844 BP; 314 A; 540 C; 596 G; 394 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1278; DB 6; Length 1844;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-260; Indels 0; Gaps 0;  
 Matches 1278; Conservative 0; Mismatches 0;  
 1 ATGACCTTCGGCGCAGCGGCGCCCTCGGTGGTGTGCTGAACGTGGCGGCGCGCGGTAT 60  
 457 ATGACCTTCGGCGCAGCGGCGCCCTCGGTGGTGTGCTGAACGTGGCGGCGCGCGGTAT 516  
 61 TGGCTGTCCGGGAGCTGCTGAGGACTTCCCGCTCCCGCGGTGAGCGGCTGACGGC 120  
 517 TGGCTGTCCGGGAGCTGCTGAGGACTTCCCGCTCCCGCGGTGAGCGGCTGACGGC 576  
 121 TGGCGCTCCGAGCGGAGCGTGTCTCAGGTGTGCGACGACTACGACCGGAGCGCAACGAG 180  
 577 TGGCGCTCCGAGCGGAGCGTGTCTCAGGTGTGCGACGACTACGACCGGAGCGCAACGAG 636  
 181 TACTTCTTCGACCGGAGCTCGGAGCGCTTCGGCTTCATCTGCTCTAGTGGCGGCCAC 240  
 637 TACTTCTTCGACCGGAGCTCGGAGCGCTTCGGCTTCATCTGCTCTAGTGGCGGCCAC 696  
 241 GCGAGAGCTGCGCTTCGGCGCGGAGTGTGCGAGCTCTCTCTTACAAAGAGATGATCTAC 300  
 697 GCGAGAGCTGCGCTTCGGCGCGGAGTGTGCGAGCTCTCTCTTACAAAGAGATGATCTAC 756  
 301 TGGGGCTTCGAGCGGCGGCGCACTTCGAGTACTGCTCCAGCGCGCGCTTCGACACCGCATG 360  
 757 TGGGGCTTCGAGCGGCGGCGCACTTCGAGTACTGCTCCAGCGCGCGCTTCGACACCGCATG 816  
 361 TCGACACCTACACTTCTTACTTCGCGCGGAGCGCGGCGGCTGCGCGCGGAGCGG 420  
 817 TCGACACCTACACTTCTTACTTCGCGCGGAGCGCGGCGGCTGCGCGCGGAGCGG 876  
 421 CGCGCGCGGCGGCGGAGCGGCTCCCTCCAGCGCGTGGCTGAGCGGATGCGGCGGAGC 480  
 877 CGCGCGCGGCGGCGGAGCGGCTCCCTCCAGCGCGTGGCTGAGCGGATGCGGCGGAGC 936  
 481 TTCGAGGAGCCACGCTGCTGCTGGCGCGGAGATCTCGGTAGCGGTGCGGTGCTGTC 540  
 937 TTCGAGGAGCCACGCTGCTGCTGGCGCGGAGATCTCGGTAGCGGTGCGGTGCTGTC 996

QY 541 GTGATCGTGTCCATGGTGGTGTGTCGCCAGCAGCAGCTTGCCTGACCTGGCGCAGCAGCC 600  
 DB 997 GTGATCGTGTCCATGGTGGTGTGTCGCCAGCAGCAGCTTGCCTGACCTGGCGCAGCAGCC 1056  
 QY 601 GCCGACAAACCGCAGCCTGGATGACCGGAGCAGGATAAATTGAAGCTATCTGCATAGGTTGG 660  
 DB 1057 GCCGACAAACCGCAGCCTGGATGACCGGAGCAGGATAAATTGAAGCTATCTGCATAGGTTGG 1116  
 QY 661 TTCACCTGCCGAGTGCATCGTGGTGGTTCATGTCCTCCAAAACAAGAGTGGTGGTTCGAAG 720  
 DB 1117 TTCACCTGCCGAGTGCATCGTGGTGGTTCATGTCCTCCAAAACAAGAGTGGTGGTTCGAAG 1176  
 QY 721 AGACCCCTGAAACATCATTTGATTTTACTGGCAATCACGCCGATTTACATCTCTGTGTTGATG 780  
 DB 1177 AGACCCCTGAAACATCATTTGATTTTACTGGCAATCACGCCGATTTACATCTCTGTGTTGATG 1236  
 QY 781 ACAGTGTTCACGCGGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGGGTACTT 840  
 DB 1237 ACAGTGTTCACGCGGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGGGTACTT 1296  
 QY 841 AGAATGATGAGGATTTTGGGGTGAATTAAGCTTGGCCGTCACCTTCAATGGTCTTCAGACA 900  
 DB 1297 AGAATGATGAGGATTTTGGGGTGAATTAAGCTTGGCCGTCACCTTCAATGGTCTTCAGACA 1356  
 QY 901 CTCGGTTTGACTCTCAAAAGTTCCTACCGAGAGATGGTATGTTACTGTGCTTCATTGTTGT 960  
 DB 1357 CTCGGTTTGACTCTCAAAAGTTCCTACCGAGAGATGGTATGTTACTGTGCTTCATTGTTGT 1416  
 QY 961 GTTGGCATGGCAATCTTTAGTGCACATTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1020  
 DB 1417 GTTGGCATGGCAATCTTTAGTGCACATTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1476  
 QY 1021 ACATCCAAACAGGACTTTTACGACATTTCTGCTGCTGCTGCTGGTGGTGAATTTCTCTATG 1080  
 DB 1477 ACATCCAAACAGGACTTTTACGACATTTCTGCTGCTGCTGCTGGTGGTGAATTTCTCTATG 1536  
 QY 1081 ACTACAGTTGGCTATGGAGATATGATCTCTATCAGAGTGCCTGGAGAAATCTTGGAGGA 1140  
 DB 1537 ACTACAGTTGGCTATGGAGATATGATCTCTATCAGAGTGCCTGGAGAAATCTTGGAGGA 1596  
 QY 1141 GTTGTGCTGCTCAGTGGAAATTTCTATTGGCAATTTACCTTATCTTATCTACCATPAGC 1200  
 DB 1597 GTTGTGCTGCTCAGTGGAAATTTCTATTGGCAATTTACCTTATCTTATCTACCATPAGC 1656  
 QY 1201 TTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGAGGCTCTCC 1260  
 DB 1657 TTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGAGGCTCTCC 1716  
 QY 1261 ACTGAATTCCTGAATTA 1278  
 DB 1717 ACTGAATTCCTGAATTA 1734

RESULT 3  
 ABZ24711  
 ID ABZ24711 standard; cDNA; 1947 BP.  
 XX AC ABZ24711;  
 XX DT 07-APR-2003 (first entry)  
 XX DE Human potassium channel subunit Kv10.1 cDNA.  
 XX KW Potassium channel; Kv10.1; human; anticonvulsant; antiarrhythmic;  
 XX KW tranquilizer; cytostatic; virucide; neuroprotective;  
 XX KW epilepsy; long QT syndrome; muscular ataxia; arrhythmia; gene therapy;  
 XX OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 596..1906  
 FT CDS



RESULT 4  
 ADD01447  
 ID ADD01447 standard; cDNA; 5174 BP.  
 XX  
 AC ADD01447;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human TCHI36 cDNA sequence.  
 XX  
 XX ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; neurotropic;  
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
 KW cytotactic; antiasthmatic; antiarthritic; cerebroprotective;  
 KW antiallergic; dermatological; cardiatic; antiParkinsonian; neuroleptic;  
 KW glucose transporter; potassium ion channel protein; diabetes;  
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;  
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;  
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;  
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;  
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003054190-A1.  
 XX  
 XX 03-JUL-2003.  
 PD  
 PF 19-DEC-2002; 2002WO-JP013290.  
 XX  
 XX 21-DEC-2001; 2001JP-00389361.  
 PR 25-DEC-2001; 2001JP-00392577.  
 PR 26-DEC-2001; 2001JP-00394947.  
 PR 26-DEC-2001; 2001JP-00395467.  
 PR 06-FEB-2002; 2002JP-00030010.  
 PR 08-FEB-2002; 2002JP-00033095.  
 PR 06-JUN-2002; 2002JP-00165336.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 PI Nakanishi A, Sagiya Y, Uno Y;  
 XX  
 DR WPI; 2003-541817/51.  
 XX  
 XX Glucose transporter TCH099, vesicular glutamate transporter TCHI77 and  
 PT potassium channel protein TCHI36 and DNA encoding them for diagnosis,  
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and  
 PT digestive disorders.  
 XX  
 PS Claim 62; SEQ ID NO 83; 221pp; Japanese.  
 XX  
 XX The invention relates to a novel glucose transporter TCH099, vesicular  
 CC glutamate transporter TCHI77 and voltage-dependent potassium ion channel  
 CC protein TCHI36. The sequences are useful in the treatment, prevention and  
 CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,  
 CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,  
 CC gastritis, ileitis and rectal inflammation), inflammatory diseases,  
 CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,  
 CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as  
 CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),  
 CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and  
 CC atopic dermatitis), circulatory disorders (such as heart failure), cancer  
 CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,  
 CC pancreas, bladder, breast, fallopian tubes or colon), central nervous  
 CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and  
 CC secretory disorders (such hyperprolactinemia and Cushing's disease). This  
 CC sequence represents the cDNA sequence for the novel human voltage-gated  
 XX potassium ion channel protein TCHI36.  
 XX  
 XX Sequence 5174 BP; 1335 A; 1139 C; 1257 G; 1443 T; 0 U; 0 Other;

Query Match 96.6%; Score 1235; DB 9; Length 5174;  
 Best Local Similarity 97.5%; Pred. No. 4.6e-251;  
 Matches 1278; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
 QY 1 ATGACCTTCGGGCGAGCGGGCGGCTCGGTGGTCTGAACTGGCGCGCGCCCGGTAT 60  
 DB 485 ATGACCTTCGGGCGAGCGGGCGGCTCGGTGGTCTGAACTGGCGCGCGCCCGGTAT 544  
 QY 61 TCCTGTTCGGGAGCTGCTGAAGGACTTCCTCCGCTCGCGCGCTGAGCCGGCTGACGGC 120  
 DB 545 TCCTGTTCGGGAGCTGCTGAAGGACTTCCTCCGCTCGCGCGCTGAGCCGGCTGACGGC 604  
 QY 121 TGGCGCTCGGAGCGGACGCTGCTGAGGCTGCGGAGCTACGACCGGAGCGCAAGGAG 180  
 DB 605 TGGCGCTCGGAGCGGACGCTGCTGAGGCTGCGGAGCTACGACCGGAGCGCAAGGAG 664  
 QY 181 TACTTCTTCACCGGCACTCGGAGGCTTCGGGCTTCATCTGCTCTACTGCGCGCCAC 240  
 DB 665 TACTTCTTCACCGGCACTCGGAGGCTTCGGGCTTCATCTGCTCTACTGCGCGCCAC 724  
 QY 241 GGAAGCTGGCTTCGGCGCGGAGTGGGAGCTCTCTTCTACACGAGATGATCTAC 300  
 DB 725 GGAAGCTGGCTTCGGCGCGGAGTGGGAGCTCTCTTCTACACGAGATGATCTAC 784  
 QY 301 TGGGGCTGGAGGGCGGCGACCTCGAGTACTGTGCGAGCGCGGCTTCGACGACCGCATG 360  
 DB 785 TGGGGCTGGAGGGCGGCGACCTCGAGTACTGTGCGAGCGCGGCTTCGACGACCGCATG 844  
 QY 361 TCGGACACTACACTTCTACTCGGCGGAGCGGCTCGGAGCTGCTGGGCGCGGAGCGG 420  
 DB 845 TCGGACACTACACTTCTACTCGGCGGAGCGGCTCGGAGCTGCTGGGCGCGGAGCGG 904  
 QY 421 CGCCCGGCGGCGGCGGAGCGGCTCGGAGCTGCTGGGCGGAGCGGAGCGGAGCGG 480  
 DB 905 CGCCCGGCGGCGGCGGAGCGGCTCGGAGCTGCTGGGCGGAGCGGAGCGGAGCGG 964  
 QY 481 TTCGAGGAGCGGCGGCTGCTGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 DB 965 TTCGAGGAGCGGCGGCTGCTGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1024  
 QY 541 GTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 DB 1025 GTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1084  
 QY 601 GCCGACAAACCGGAGCTGAGTACCGGAGCA----- 631  
 DB 1085 GCCGACAAACCGGAGCTGAGTACCGGAGCAAGTACTCCCGCGGCGCTGGGAGGAGCC 1144  
 QY 632 -----GGATAATTGAAGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687  
 DB 1145 TCGGGATAATTGAAGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204  
 QY 688 ATTGCTCCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTACTG 747  
 DB 1205 ATTGCTCCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTACTG 1264  
 QY 748 GCAATACGCGGCTATTACATCTCTGTTGTGATGACAGTGTGTTTACAGCGGAGAACTCTCAA 807  
 DB 1265 GCAATACGCGGCTATTACATCTCTGTTGTGATGACAGTGTGTTTACAGCGGAGAACTCTCAA 1324  
 QY 808 CTCGAGGAGGCTGGAGTACCTTGAAGGTACTTAGATGATGAGGATTTTTCGGTGAAT 867  
 DB 1325 CTCGAGGAGGCTGGAGTACCTTGAAGGTACTTAGATGATGAGGATTTTTCGGTGAAT 1384  
 QY 868 AAGCTTCCCGCTCACATTTCAATTTGCTTTCAGACACTCGGTTTGTACTCTCAAACCTTGTCTAC 927  
 DB 1385 AAGCTTCCCGCTCACATTTCAATTTGCTTTCAGACACTCGGTTTGTACTCTCAAACCTTGTCTAC 1444  
 QY 928 CGAGAGATGTTTATGTTTACTTGTCTTCTTCTTGTGTCGCAATCTTTAGTGCACTT 987  
 DB 1445 CGAGAGATGTTTATGTTTACTTGTCTTCTTCTTGTGTCGCAATCTTTAGTGCACTT 1504











PI	Pattarajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD;
PI	Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;
PI	Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W;
PI	Anderson DW, Leite NW, Rastelli L, Edinger SR, Stone DJ;
PI	Maddougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
PI	Ellerman K;
XX	
DR	WFI: 2003-046858/04.
XX	P-PSDB: ABU54564.
XX	
PT	New isolated NOVX polypeptide useful for treating atherosclerosis,
PT	metabolic disorders, diabetes, obesity, infectious disease, anorexia,
PT	neurodegenerative disorders, Alzheimer's disease and cancer.
XX	
PS	Claim 17; Page 136; 66pp; English.
XX	
CC	The invention relates to human polypeptides, termed NOVX, and the
CC	polynucleotides encoding them. The polypeptides and polynucleotides are
CC	useful for diagnosing disease, and screening for potential therapeutic
CC	agents. The sequences are useful for treating metabolic disorders, aortic
CC	cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
CC	stenosis, atrial septal defect (ASD), atriocutricular canal defect,
CC	ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
CC	septal defect (VSD), valve diseases, tuberosus sclerosis, scleroderma,
CC	atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
CC	disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC	haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
CC	and cancer. Sequences ABX72170-ABX72275 represent human NOVX
CC	polynucleotides of the invention
XX	
SQ	Sequence 1651 BP; 292 A; 476 C; 510 G; 373 T; 0 U; 0 Other;

	Query Match	86.0%	Score 1099.4	DB 7	Length 1651	
	Best Local Similarity	91.4%	Pred. No. 1.6e-222			
	Matches 1231	Conservative	0	Mismatches 11	Indels 105	Gaps 2
QY	1	ATGACCTTTGGCGCAGCGGGCGGCTCGTGTGTGTGAACATGGCGCGCCCGCGGTAT	60			
Db	58	ATGACCTTTGGCGCAGCGGGCGGCTCGTGTGTGTGAACATGGCGCGCCCGCGGTAT	117			

61	QY	TGCGTGTCCGGGAGCTGTGAAGACTTCCGCTGCGCGCGTAGCGGGCTGCACGCG	120
118	Db	TGCGTGTCCGGGAGCTGTGAAGACTTCCGCTGCGCGCGTAGCGGGCTGCACGCG	177
121	QY	TGCGGCTCGAGCGCGAAGTGCTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	180
178	Db	TGCGGCTCGAGCGCGAGCTGTCTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG	237
181	QY	TACTTCTTCGACCGGCACTCGAGAGCCTTCGGCTTTCATCTGTCTACGTGCGCGGCCAC	240
238	Db	TACTTCTTCGACCGGCACTCGAGAGCCTTCGGCTTTCATCTGTCTACGTGCGCGGCCAC	297
241	QY	GGGAGACTGCGCTTCGCGCCCGGATGTGCGAGCTCTCTTTACAAAGAGATGATCTAC	300
298	Db	GGCAAGACTGCGCTTCGCGCCCGGATGTGCGAGCTCTCTTTACAAAGAGATGATCTAC	357
301	QY	TGGGGCTGGAGGGCGCGACCTCGAGTACTGTGTGCCAGCGCGCGCTTCGACACCGCATG	360
358	Db	TGGGGCTGGAGGGCGCGACCTCGAGTACTGTGTGCCAGCGCGCGCTTCGACACCGCATG	417
361	QY	TCCGACACTACACTTCTACTCGGCGGACGAGCCGGGCGTGTGTGGCGCGCGACGAGGGC	420
418	Db	TCCGACACTACACTTCTACTCGGCGGACGAGCCGGGCGTGTGTGGCGCGCGACGAGGGC	477
421	QY	CGCCCGCGGGGGCG-----	434
478	Db	CGCCCGCGGGCGGAGCGGCTCTCTCAGCGCTGGCTGGAGCGCATGCGCGGACCTT	537
435	QY	-----CGAGCGGCTCTCTCAGCGGCTGGCTGGAGCGCATGCGCGGACCTTC	483
538	Db	CGAGAGAGCCCACTGTCTGCTGGCGGAGGGCGTGGCTGTGAGGCGCATGCGGCGGACCTTC	597
484	QY	GAGGAGAGCCCACTGTCTGCTGGCGGCGCGAGATCTGTGCTAGCGTGTCTGTGTGTCTGTG	543

Db	598	GAGGAGCCACGTCGTGCGTGGCGCGCACATCTGTGCTAGCGTGTGCGTGGTGTTCGTG	657
Qy	544	ATCGTGTCATGTTGGTGTGCGCGCAGACAGTTCGCCAGCTGGCGCAACGACGCGGCC	603
Db	658	ATCGTGTCATGTTGGTGTGCGCGCAGACAGTTCGCCAGCTGGCGCAACGACGCGGCC	717
Qy	604	GACAAACGCGCCTGGATGACCGGAG	629
Db	718	GACAAACGCGCCTGGATGACCGGAGCAGGTA	777
Qy	630	-----CAGGATAATTGAAGCTTATCTGCATAGGTTGGTCACTCCGCGAGCCCTCC	675
Db	778	GGGTGTTCTTTGACAGGATAATTGAAGCTTATCTGCATAGGTTGGTCACTCCGCGAGTGC	837
Qy	676	ATCGTGAGGTTCAATTGTCTCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATC	735
Db	838	ATCGTGAGGTTCAATTGTCTCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATC	897
Qy	736	ATTGATTTACTGGAATCAGCCGATATACATCTCTGTGTTGATGACAGTGTTCAGGC	795
Db	898	ATTGATTTACTGGAATCAGCCGATATACATCTCTGTGTTGATGACAGTGTTCAGGC	957
Qy	796	GAGAACTCTCAACTCCAGAGGGCTGGAGTCACCTTCAGGGTACTTGAATGATGAGGATT	855
Db	958	GAGAACTCTCAACTCCAGAGGGCTGGAGTCACCTTCAGGGTACTTGAATGATGAGGATT	1017
Qy	856	TTTTGGGTGATTAAAGCTTGGCCGTCATCTCAATTTGGTCTTCAGACACCTCGGTTTGA	915
Db	1018	TTTTGGGTGATTAAAGCTTGGCCGTCATCTCAATTTGGTCTTCAGACACCTCGGTTTGA	1077
Qy	916	AAACGTTGCTACCGAGAGATGGTTATGTTACTTTGTCCTTCAATTTGTTGCCATGGCAATC	975
Db	1078	AAACGTTGCTACCGAGAGATGGTTATGTTACTTTGTCCTTCAATTTGTTGCCATGGCAATC	1137
Qy	976	TTTAGTGCACTTCTCAGCTTCTTGAACTTTGAACTGGCGCTGGAACATCCAAACAAGGAC	1035
Db	1138	TTTAGTGCACTTCTCAGCTTCTTGAACTTTGAACTGGCGCTGGAACATCCAAACAAGGAC	1197
Qy	1036	TTTACCAGCAATTCCTGCTGCTGCTGGTGGGTGATTATCTCTATGACTACAGTTGGCTAT	1095
Db	1198	TTTACCAGCAATTCCTGCTGCTGCTGGTGGGTGATTATCTCTATGACTACAGTTGGCTAT	1257
Qy	1096	GGAGATATGTATCCTATCACAGTGCCTTGGAAAGAAATCTTTGGAGGAGTTTGTGTGTCAGT	1155
Db	1258	GGAGATATGTATCCTATCACAGTGCCTTGGAAAGAAATCTTTGGAGGAGTTTGTGTGTCAGT	1317
Qy	1156	GGAAATGTTCTATGCGAATACCTATCAGCTTTTATCTACATAGAGCTTTGGCAGTGTAT	1215
Db	1318	GGAAATGTTCTATGCGAATACCTATCAGCTTTTATCTACATAGAGCTTTGGCAGTGTAT	1377
Qy	1216	CATGAGCTCAAGTTTAGATCTGCTAGG	1242
Db	1378	CATGAGCTCAAGTTTAGATCTGCTAGG	1404
RESULT 8			
ABZ24716			
ID	ABZ24716	standard; cdna; 5775 BP.	
XX	AC	ABZ24716;	
XX	AC	ABZ24716;	
DT	07-APR-2003	(first entry)	
XX	DE	Murine potassium channel subunit Kv10.1 - flag sequence.	
XX	XX	Potassium channel; Kv10.1; mouse; transgenic mouse; gene; ss.	
XX	XX	Mus musculus.	
OS	XX		
Key	XX	Location/Qualifiers	
FT	FT	misc_feature	3424..4749
FT	FT	/*tag= a	

DECLASS. AUTHORITY

RESOLUTION  
ABZ24716

ADZ1110  
TD ARZ.

[illegible]

AC ABZ



DT 07-

XX

DE Mur

XX

KW Pot

XX :

OS Mus

XXIII

Key	Value
EH	0
Key	0

STIM

—

10

—

FT XX /note= "flag"  
 PN XX WO200296944-A2.  
 XX PD 05-DEC-2002.  
 XX PF 31-MAY-2002; 2002WO-EP006082.  
 XX PR 31-MAY-2001; 2001EP-00202060.  
 XX PA (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 XX PI Snyders DJ, Otschysch N, Raes A, Van Hoorick D;  
 XX DR WPI; 2003-140443/13.  
 XX PT Novel voltage-gated heterotetrameric potassium channel useful for  
 PT diagnosing, preventing and/or treating excitability disorders, comprises  
 PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.  
 XX Example; Page 80-82; 93pp; English.  
 XX The present sequence is that of a construct used in the creation of a  
 CC potassium channel subunit Kv10.1 transgenic mouse. In an example from the  
 CC invention, the construct was microinjected into the pronucleus of a one-  
 CC cell embryo, and then incubated in a foster mother of the FVB/Nlco mouse  
 CC strain. The invention provides novel, voltage-gated heterotetrameric  
 CC potassium channels comprising Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or  
 CC Kv11.1. These are useful for identifying a molecule that increases or  
 CC decreases ion flux through the potassium channel (claimed). Nucleic acids  
 CC encoding the heterotetrameric potassium channels are used in gene therapy  
 CC to prevent or treat congenital or acquired excitability disorders  
 CC including epilepsy, long QT syndrome, muscular ataxia, and arrhythmia  
 CC (all claimed)  
 XX SQ Sequence 5775 BP; 1327 A; 1530 C; 1532 G; 1386 T; 0 U; 0 Other;  
 Query Match 83.7%; Score 1070; DB 7; Length 5775;  
 Best Local Similarity 90.3%; Pred. No. 3.2e-216;  
 Matches 1183; Conservative 0; Mismatches 85; Indels 42; Gaps 2;  
 QY 1 ATGACCTTCGGCGAGCGGGCGGCTCGTGGTCTGAACGTTGGCGCGCGCGGTAT 60  
 DB 3424 ATGACCTTCGGCGAGCGGGCGGCTCGTGGTCTGAACGTTGGCGCGCGCGGTAC 3483  
 QY 61 TCCTCTCCCGGAGCTGCTGAAGACTTCCGCTCGCGCGGCTGAGCGCGGTGCAACGCG 120  
 DB 3484 TCCTCTCCCGGAGCTGCTGAAGACTTCCGCTCGCGCGGCTGAGCGCGGTGCAACGCG 3543  
 QY 121 TGCGGCTTCGAGCGCGAGCTGCTCGAGGTGTGCGAGCTACGACCGGAGCGCAACGAG 180  
 DB 3544 TGCGGCTTCGAGCGCGAGCTGCTCGAGGTGTGCGAGCTACGACCGGAGCGCAACGAG 3603  
 QY 181 TACTTCTTCGAGCGCGAGCTGCGAGGCTTCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
 DB 3604 TACTTCTTCGAGCGCGAGCTGCGAGGCTTCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 3663  
 QY 241 GGCAAGCTGGCTTCGCGCGCGGAGTGTGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
 DB 3664 GGCAAGCTGGCTTCGCGCGCGGAGTGTGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3723  
 QY 301 TGGGGCTTCGAGCGCGGAGCTGCTGAGTGTGCTGCGAGCGCGGCTTCGACCGCGCATG 360  
 DB 3724 TGGGGCTTCGAGCGCGGAGCTGCTGAGTGTGCTGCGAGCGCGGCTTCGACCGCGCATG 3783  
 QY 361 TCGGACCTTACACCTTCTACTCGCGCGAGCGCGGCGGTGCTGGCGCGCGAGCGAGCGG 420  
 DB 3784 TCGGACCTTACACCTTCTACTCGCGCGAGCGCGGCGGTGCTGGCGCGCGAGCGAGCGG 3834  
 QY 421 CGCGCGCGCGCGCGAGCGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
 DB 3835 CGTCCGCGCGAGCGCGAGCGCGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3894

QY 481 TTCAGAGAGCCAGCTGCTGCTGCGCGCGAGATCCTGGCTAGCTGCTGCTGCTGCTGCTGCTGCT 540  
 DB 3895 TTCAGAGAGCCAGCTGCTGCTGCGCGCGAGATCCTGGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3954  
 QY 541 GTGATCGTGTCCATGCTGCTGCTGCGCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 DB 3955 GTGATCGTGTCCATGCTGCTGCGCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4014  
 QY 601 GCGGACAAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 631  
 DB 4015 GCTGACAAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4074  
 QY 632 ----GGATAATTGAAGCTATCTGCTAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687  
 DB 4075 TCGGGATAATTGAAGCTATCTGCTAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4134  
 QY 688 ATTGTCTCCAAAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 747  
 DB 4135 ATCGTCTCCAAAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4194  
 QY 748 GCAATCAGCGCGTATACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 807  
 DB 4195 GCAATCAGCGCGTATACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4254  
 QY 808 CTCAGAGGGCTGAGTCACTTGGAGTCTTAGAATGATGAGGATTTTTCGGGTGATT 867  
 DB 4255 CTCAGAGGGCTGAGTCACTTGGAGTCTTAGAATGATGAGGATTTTTCGGGTGATT 4314  
 QY 868 AAGTTCGCGCT 927  
 DB 4315 AAGTTCGCGCT 4374  
 QY 928 CGAGAGATGCT 987  
 DB 4375 CGAGAGATGCT 4434  
 QY 988 TCTCAGTCTTCTGAAATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1047  
 DB 4435 TCTCAGTCTTCTGAAATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 4494  
 QY 1048 CCTGCT 1107  
 DB 4495 CCTGCT 4554  
 QY 1108 CCTATCAGTGTGCT 1167  
 DB 4555 CCTATCAGTGTGCT 4614  
 QY 1168 TTGGCATTTACCTATCTGCT 1227  
 DB 4615 TTGGCATTTACCTATCTGCT 4674  
 QY 1228 TTTAGATCTGCTAGGATAGTAGGAGCTCTCCAGTGAATTCCTGGAATTA 1277  
 DB 4675 TTTAGATCTGCTAGGATAGTAGGAGCTCTCCAGTGAATTCCTGGAATTA 4724  
 RESULT 9  
 AAD33662  
 ID AAD33662 standard; cDNA; 2312 BP.  
 XX  
 AC AAD33662;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Human TRICH-17 cDNA.  
 XX  
 KW Human; transporter and ion channel; TRICH-17; transport disorder; angina;  
 KW amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;  
 KW cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;  
 KW depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;  
 KW cell proliferated disorder; infertility; arteriosclerosis; gene therapy;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;

KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;  
KW acquired immune deficiency syndrome; immunological disorder; scleroderma;  
KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;  
KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;  
KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;  
KW muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;  
KW gene, ss.  
XX  
XX Homo sapiens.  
OS

XX Key Location/Qualifiers  
FH 325..1845  
FT CDS /\*tag= a  
FT /\*product= "Human TRICH-17 protein"  
XX  
XX W0200212340-A2.  
XX  
XX 14-FEB-2002.  
XX

XX 01-AUG-2001; 2001W0-US024217.  
XX  
XX 03-AUG-2000; 2000US-0223269P.  
XX 10-AUG-2000; 2000US-0224456P.  
XX 18-AUG-2000; 2000US-0226410P.  
XX 25-AUG-2000; 2000US-0228140P.  
XX 31-AUG-2000; 2000US-0230067P.  
XX 08-SEP-2000; 2000US-0231434P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX

XX Yue H, Thornton M, Ramkumar J, Tang Y, Azimzai Y, Baughn MR;  
PI Yang J, Yao MG, Lal P, Walia NK, Gandhi AR, Hafalia AJA, Nguyen DB;  
PI Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;  
PI Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;  
PI Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;  
PI Das D, Kallick DA, Khan FA, Seilhamer JJ;  
XX WPI; 2002-206330/26.  
DR P-PSDB; AAE21173.  
XX

XX New human transporters and ion channels polypeptides and polynucleotides  
PT for diagnosing, preventing or treating transport, neurological, muscle,  
PT immunological and cell proliferative disorders.  
XX  
XX Claim 91; Page 217; 230pp; English.

XX The invention relates to human transporter and ion channel polypeptides  
CC designated TRICH and nucleic acid molecules encoding such polypeptides.  
CC TRICH sequences are useful for diagnosis, treatment and prevention of  
CC transport, muscle, neurological, immunological and cell proliferative  
CC disorders. Transport disorders include akinesia, amyotrophic lateral  
CC sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular  
CC dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,  
CC myocarditis, prostate cancer, cardiac disorders associated with transport  
CC e.g. polymyositis, bradyarrhythmia, dermatomyositis, angina, neurological  
CC disorders associated with transport e.g. amnesia, bipolar disorder,  
CC depression, Tourette's disorder, schizophrenia, other disorders  
CC associated with transport e.g. neurofibromatosis, sickle cell anaemia,  
CC Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,  
CC goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell  
CC proliferated disorders include cancer, actinic keratosis, cirrhosis,  
CC arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.  
CC Neurological disorders include Alzheimer's, Pick's and Parkinson's  
CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's  
CC disease, multiple sclerosis, dementia and other extrapyramidal disorder,  
CC motor neuron disorder, prion disease, metabolic disease of the nervous  
CC system and other developmental disorders of the central nervous system,  
CC neuromuscular disorders, metabolic, endocrine and toxic myopathies,  
CC periodic paralysis, mental disorders including mood, anxiety; and  
CC immunological disorders include acquired immune deficiency syndrome  
CC (AIDS), adult respiratory distress syndrome, Addison's disease,  
CC allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,

CC Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,  
CC systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,  
CC haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal,  
CC helminthic infections and trauma, and muscle disorders include cardiac  
CC myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The  
CC TRICH polynucleotides are used in gene therapy. The present sequence is  
CC human TRICH-17 cDNA  
XX  
XX Sequence 2312 BP; 475 A; 607 C; 674 G; 556 T; 0 U; 0 Other;

XX Query Match 66.2%; Score 846.6; DB 6; Length 2312;  
XX Best Local Similarity 93.3%; Pred. No. 4e-169;  
XX Matches 885; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

XX  
QY 330 CTGCTGCCAGCGCGCCCTCGACGACCGCCTGTCGACACCTTCTACTCGGCGGA 389  
DB 897 CTGCGCTCGAGCGCGAGCTGCTCGAGGTGTGCGACGACTACGCCGCGCACAGA 956  
QY 390 CGAGCGCGGCGTGTGGCGCGCGACGAGGCGCGCGCGCGCGCGCGCGCGCGCG 449  
DB 957 GTACTTTCTGACCGGCACCTCGAGGCGCTTCGGGCTTCATCTGCTACGCGGCTCCTC 1016  
QY 450 CAGGCGCTGGCTGGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTCGCTGGCGCG 509  
DB 1017 CAGGCGCTGCTGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTGCTGCGCGCG 1076  
QY 510 GCAGATCCTGCTAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569  
DB 1077 GCAGATCCTGCTAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1136  
QY 570 CAGCACCTGCTCGGACCTGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 629  
DB 1137 CAGCACCTGCTCGGACCTGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1196  
QY 630 CAGGATAATGAAGCTATCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689  
DB 1197 CAGGATAATGAAGCTATCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1256  
QY 690 TGCTCCAAAAACAAGTGTGAGTTTCAAGAGACCCCTGAAACATCATTTGATTTACTGGC 749  
DB 1257 TGCTCCAAAAACAAGTGTGAGTTTCAAGAGACCCCTGAAACATCATTTGATTTACTGGC 1316  
QY 750 AATCACCCCTATTACATCTCTGTTGATGACAGTGTGTTACAGGCGAGAACTCTCAACT 809  
DB 1317 AATCACCCCTATTACATCTCTGTTGATGACAGTGTGTTACAGGCGAGAACTCTCAACT 1376  
QY 810 CCAGAGGCTGGAGTCACTTGGAGGTACTTAAATGATGAGGATTTTGGGTGATTA 869  
DB 1377 CCAGAGGCTGGAGTCACTTGGAGGTACTTAAATGATGAGGATTTTGGGTGATTA 1436  
QY 870 GCTTGCCCGTCACTTCACTTGGCTTTCAGACACTCGGTTTGAATCTCAAAAGTTGCTACCG 929  
DB 1437 GCTTGCCCGTCACTTCACTTGGCTTTCAGACACTCGGTTTGAATCTCAAAAGTTGCTACCG 1496  
QY 930 AGAGATGGTTATCTTACTTGTCTTCAATTTGTTGCTGCGCAATCTTTAGTGCATTTTC 989  
DB 1497 AGAGATGGTTATCTTACTTGTCTTCAATTTGTTGCTGCGCAATCTTTAGTGCATTTTC 1556  
QY 990 TCAGCTCTTGACATGGGTGCGACCTGGAACATCCAAAGGATTTTACAGGATTC 1049  
DB 1557 TCAGCTCTTGACATGGGTGCGACCTGGAACATCCAAAGGATTTTACAGGATTC 1616  
QY 1050 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109  
DB 1617 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1676  
QY 1110 TATCAGAGTCCCTGGGAAGAAATCTTGGAGAGTTTGTGTTGTCAGTGGAAATTTCTTATT 1169  
DB 1677 TATCAGAGTCCCTGGGAAGAAATCTTGGAGAGTTTGTGTTGTCAGTGGAAATTTCTTATT 1736  
QY 1170 GGCATTACCTATCATTCTTTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTT 1229  
DB 1737 GGCATTACCTATCATTCTTTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTT 1796

QY 1230 TAGATCTGCTAGTATAGTAGGAGCCTCTCCACTGAAATCCCTGAATTA 1278  
DB 1797 TAGATCTGCTAGTATAGTAGGAGCCTCTCCACTGAAATCCCTGAATTA 1845

RESULT 10  
ADD01469  
ID ADD01469 standard; cDNA; 950 BP.  
XX  
AC ADD01469;  
XX  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Mouse TCH136 cDNA sequence fragment.  
XX  
KW ds; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;  
KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
KW cytotatic; antiasthmatic; antiarthritic; cerebroprotective;  
KW antiallergic; dermatological; cardiant; antiParkinsonian; neuroleptic;  
KW glucose transporter; potassium ion channel protein; diabetes;  
KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;  
KW meningitis; hepatitis; myocarditis; asthma; immune disorder;  
KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
KW allergy; hay fever; allergic rhinitis; anaphylactic shock;  
KW atopic dermatitis; circulatory disorder; heart failure; cancer;  
KW Alzheimer's disease; Parkinson's disease; schizophrenia;  
KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.

XX Mus sp.  
OS  
XX WO2003054190-A1.  
XX  
XX 03-JUL-2003.  
XX  
XX 19-DEC-2002; 2002WO-JP013290.  
XX  
XX 21-DEC-2001; 2001JP-00389361.  
XX 25-DEC-2001; 2001JP-00392577.  
XX 26-DEC-2001; 2001JP-00394947.  
XX 26-DEC-2001; 2001JP-00395467.  
XX 08-FEB-2002; 2002JP-00030010.  
XX 08-FEB-2002; 2002JP-00033095.  
XX 06-JUN-2002; 2002JP-00165336.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Nakanishi A, Sagiya Y, Uno Y;  
XX WPI; 2003-541817/51.  
XX  
XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and  
XX potassium channel protein TCH136 and DNA encoding them for diagnosis,  
XX treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and  
XX digestive disorders.  
XX  
XX Example 21; SEQ ID NO 105; 211pp; Japanese.  
XX  
XX The invention relates to a novel glucose transporter TCH099, vesicular  
XX glutamate transporter TCH177 and voltage-dependent potassium ion channel  
XX protein TCH136. The sequences are useful in the treatment, prevention and  
XX diagnosis of a broad range of diseases including diabetes, hyperlipemia,  
XX arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,  
XX gastritis, ileitis and rectal inflammation), inflammatory diseases,  
XX sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,  
XX meningitis, hepatitis, myocarditis, asthma, immune disorders (such as  
XX multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),  
XX allergies (such as hay fever, allergic rhinitis, anaphylactic shock and  
XX atopic dermatitis), circulatory disorders (such as heart failure), cancer  
XX (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,  
XX pancreas, bladder, breast, fallopian tubes or colon), central nervous

CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and  
CC secretory disorders (such hyperprolactinemia and Cushing's disease). This  
CC sequence represents a fragment of the cDNA sequence for the novel mouse  
CC voltage-dependent potassium ion channel protein TCH136.  
XX  
SQ Sequence 950 BP; 182 A; 263 C; 269 G; 230 T; 0 U; 6 Other;  
Query Match 57.1%; Score 729.8; DB 9; Length 950;  
Best Local Similarity 88.9%; Pred. No. 1.6e-144;  
Matches 848; Conservative 0; Mismatches 87; Indels 19; Gaps 5;  
QY 294 GATCTACTGGGGCTGAGGGCGCGACCTCGAGTACTGTCCAGCGCGCTCCACGA 353  
DB 1 GATCTACTGGGGCTGAGGGTGGCGACCTCGAGTACTGTCCAGCGCGCTCCACGA 60  
QY 354 CCGCATCTCCGACACCTACACCTTTCTACTCGGGCGAGCGCGGGCTGTGGGGCGCGA 413  
DB 61 CCGCATCTCCGACACCTTTCTACTCGGGCGAGCGA-----GCTGGGGCGCGA 111  
QY 414 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCTCCAGCGCGTGGTGAGCGCATGCG 473  
DB 112 GCAGCCTCGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGTGAGCGCATGCG 171  
QY 474 CGCGACCTTCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCATCTGGCTAGCGTGTGGT 533  
DB 172 CGCGACCTTCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCATCTGGCGCGCATCTGGT 231  
QY 534 GGTCTTCGATCTGTCATGT 593  
DB 232 GGTCTTCGATCTGTCATGT 291  
QY 594 CGCATCTGTGCAT 653  
DB 292 GCGCGTGTCTGACAAACCGCGAGTCTGGATGACCGCGCGCGCGCGCGCGCGCGCGCAT 351  
QY 654 AGGTGTGTCTACCTCCCGAGTGCATCTGTAGGTTCATTTGTCTCCAAACAAAGTGTGAGTT 713  
DB 352 AGGTGTGTCTACCTCCCGAGTGCATCTGTGGGTTCATCTGTCTCCAAACAAAGTGTGAGTT 411  
QY 714 TGTCAAGAGACCCCTGACATCATTTGATTTACTGGCAATCACGCGCTATTACATCTCTGT 773  
DB 412 TGTCAAGAGACCCCTGACATCATTTGATTTACTGGCAATCACGCGCTATTACATCTCTGT 471  
QY 774 GTTGTATGACAGTGTATACAGCGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTTGAG 833  
DB 472 GCTAATGACAGTGTATACAGCGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTTGAG 531  
QY 834 GGTACTTGAATGATGAGGATTTTGTGGGTGATTAAGCTTTCCTGCTGCTGCTGCTGCTGCT 893  
DB 532 GGTCTCCGAATGATGCGGATCTTCTGGGTGATCAAGCTTGGCGCGCTTCTGCTGCTGCT 591  
QY 894 TCAGACACTCGTTTGTACTCTCAACCGTTGCTACCGAGAGATGTTATGTTACTTGTCTT 953  
DB 592 GCAGACACTGGCTTGTACTCTCAAGCGATGCTACCGAGAGATGCTATGTTACTTGTCTT 651  
QY 954 CATTGTGTTGCCATGGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAACAATGGCTGGA 1013  
DB 652 CATCTGTGTTGCCATGGCAATCTTTAGTGCACTCTCTCAGCTCTCTGAGCAATGGCTGGA 711  
QY 1014 CCTGAAATCCCAACAGGACTTTTACCAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073  
DB 712 CCTGAAATCCCAACAGGACTTTTGGCGAGCATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 771  
QY 1074 CTCTATGACTACAGTGGCTATGAGATATATATCTTATCTACAGTGGCTGCTGCTGCTGCTGCT 1133  
DB 772 CTCTATAACTACAGTGGCTATGAGATATATATCTTATCTACAGTGGCTGCTGCTGCTGCTGCT 831  
QY 1134 TGG---AGAGT 1186  
DB 832 TGGNAGAGAGT 891  
QY 1187 TTAT-CTACCATAGCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1237

Db 892 TCATCCTACCATAGCTTTGTGAGTGTCTACACGAGGCTCAAGTTTATGATCGG 945

RESULT 11

ABQ49122

ID ABQ49122 standard; DNA; 1634 BP.

XX AC ABQ49122;

XX DT 12-JUL-2002 (first entry)

XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 35713.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX drug; side effect; cancer; central nervous system; cardiovascular;

XX gastrointestinal; respiratory system; single nucleotide polymorphism;

XX SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.

XX PD 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIC-) EPIDENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful for

XX diagnosis and prognosis, comprises selective hybridization of amplicons

XX from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of

XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a

XX genomic sample of DNA. The sample is treated chemically to convert

XX cytosine (C) but not methylated C, to uracil, then part of the genomic

XX DNA that contains the target C is amplified to form a labeled amplicon.

XX The amplicon is hybridised to two classes, each with at least one member,

XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

XX degree of hybridisation to both classes is determined from the label on

XX the amplicon. From the ratio of labels hybridised to the two classes of

XX oligomers, the degree of methylation is calculated. The method is used:

XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs

XX and of a wide range of diseases, e.g. cancer, disorders of the central

XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

XX particularly by detecting mutations or single nucleotide polymorphisms

XX (SNPs); and (ii) for differentiation of cell or tissue types and for

XX investigating cell differentiation. The method allows the methylation

XX status of many C residues to be determined simultaneously. ABQ13410-

XX ABQ54121 represent genomic DNA sequences used to illustrate the method

XX for determining the degree of cytosine methylation described in the

XX disclosure of the invention

XX SQ Sequence 1634 BP; 212 A; 232 C; 624 G; 566 T; 0 U; 0 Other;

Query Match 31.8%; Score 406.6; DB 6; Length 1634;

Best Local Similarity 77.8%; Pred. No. 3e-76;

Matches 516; Conservative 0; Mismatches 144; Indels 3; Gaps 2;

QY 1 ATGACCTTCGGGGGACGGGGGGGGCTCGGTGGTCTGAACGTGGGGGGCCCGGTAT 60

Db 726 ATGATTTTCGGGGGTAGCGGGGGGGTTTCGTGGTTCGAACGTGGGGGGCGTTTCGTAT 785

QY 61 TGGCTCTCCGGAGGTGTGTAAGACTTCCCGCTGCCCGCGTGGAGCGGCTGACCGC 120

Db 786 TCGTTGTTCCGGAGTTGTTGAAGATTTTCGTTGCGTCCGCTGAGTCGGTTAGCGT 845

QY 121 TGCCECTCCGAGCCGAGCTGCTCGAGGTGTCGACGACTACGACCGAGCGCAACGAG 180

Db 846 TGTGCTTTCGAGCGGACGCTGTTCCAGGTGTCGACGATTACGATCGCGAGCGTAACGAG 905

QY 181 TACTTCTCGACCGGCACTCGGAGCCTTCGGCTTCATCCTGCTCTACGTCGCGGCCAC 240

Db 906 TATTTTTCGATCGGTATTCGAGGTTTCGGTTTATTTTGTGTTTACGTCGCGGTTC 965

QY 241 GCGAGCTGCGCTTCGCGCCGCGGATGTCGAGTCTCTCTTCTACAAGAGATGATCTAC 300

Db 966 GGTAACTGCGCTTCGCGG-CGCGGATGTCGAGTTTTCGTTTATAACGAGATGATTAT 1024

QY 301 TGGGCGCTGAGGCGCGGACCTCGAGTACTGCTGCCAGCGCCGCTCGACGACCGCATG 360

Db 1025 TGGGCTTGGAGGGCGGATTTTCGAGTATTTGTTAGCGTCTGTTTCGACGATCGTATG 1084

QY 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGGCGCTGCTGGGCGCGAGAGCGC 420

Db 1085 TTCGATATTTATATTTTATTCGTCGAGTCCGCGCTGTTGGTTCGCGAGAGCGC 1144

QY 421 CGCCCGCGCGGCGGAGCGGCTCCCTCCAGGCGCTGGCTGGAGCGCATCGCGCGGACC 480

Db 1145 CGTTTCGCGCGG--CGAGGCGGTTTTTTTAGGCGGTTGGTTGGAGCGTATCGCGCGGATT 1202

QY 481 TTCGAGAGCGCCACGCTGCTCGCTCGCGCGCAGATCTCGGCTAGCGTGTGGTGTTC 540

Db 1203 TTCGAGAGGTTTACGTCGCTGCTGCTGCGGTAGATTTTGTGTCGCTGCTGCTGTTTC 1262

QY 541 GTGATCGTGTCCATGCTGCTGCTGCGCGAGCAGTTCGCGCGGCTGCGCGGCGGCGGAC 600

Db 1263 GTGATCGTGTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1322

QY 601 GCCGACACCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

Db 1323 GTGATATTCGATGTTTGGATGTCGCGAGTAGTATTTTCGCTGCTGCTGCTGCTGCTGCT 1382

QY 661 TTC 663

Db 1383 TTC 1385

RESULT 12

ABQ49123/c

ID ABQ49123 standard; DNA; 1634 BP.

XX AC ABQ49123;

XX DT 12-JUL-2002 (first entry)

XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 35714.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX drug; side effect; cancer; central nervous system; cardiovascular;

XX gastrointestinal; respiratory system; single nucleotide polymorphism;

XX SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.

XX PD 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIC-) EPIDENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

PI



XX WPI; 2002-371829/40.  
XX  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
XX Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNPs); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
XX Query Match 31.88; Score 406.6; DB 6; Length 1634;  
XX Best Local Similarity 77.88; Pred. No. 3e-76;  
XX Matches 516; Conservative 0; Mismatches 144; Indels 3; Gaps 2;  
Qy 1 ATGACCTTCGGGGCGCAGCGGGCGGCTCGTGGTGTCTGAACTGGCGCGCGCCGGTAT 60  
Db 909 ATGATTTTCGGGGCGTAGCGGGCGGTTTCGTTGGTGTGAACGTGGCGCGCTCGGTAT 850  
Qy 61 TCGCTGTCCGGGAGCTGTGAAGGACTCCCGCTGGCGCGGTGAGCGCGTGCACGC 120  
Db 849 TCGTTGTTCGGGAGTGTGAAGGATTTTCGTTGGTGTGAGTTCGTTGTGACGT 790  
Qy 121 TGGCGCTCCGAGCGCGCAGCTGCTCGAGGTGTGGAGGACTACGACCGCGAGCGACGAG 180  
Db 789 TGTGTTTCGAGCGCGAGCTGTTTCGAGGTGTGCGAGGATTACGATCGCGAGGTAACGAG 730  
Qy 181 TACTTTCGACCGGCACTCGAGGCGCTTCGGCTTCTACGTCCTACGTGCGCGCCAC 240  
Db 729 TATTTTTCGATCGGTATTCGAGGTTTCGCTTTATTTTGTTCGTCGCGGTTAC 670  
Qy 241 GGCAAGCTGCGTTCGGCGCGCGAGTGTGCGAGTCTCCTCTACACGAGATGATCTAC 300  
Db 669 GGTAAAGTTGGTTTCGGG-CCGCGAGTGTGCGAGTTTATTTTATACGAGATGATTTAT 611  
Qy 301 TGGGGCTCGAGGCGCGCAGCTCGAGTAATGTGTCGAGCGCGCGCTCGACGACCGCAGT 360  
Db 610 TGGGGTTTGGAGGCGCGGTATTTTCGAGTATTTTGTGTAGCGCTGTTTCGACGATCGTATG 551  
Qy 361 TCGACACCTACACTTCTACTCGGCGCAGCGCGGCTGTGCGCGCGCAGCGAGCG 420  
Db 550 TTCCATATTTATTTTATTTTATTTGTCGACAGTGTGGGCGTGTGAGTCCGACGAGCGG 491  
Qy 421 CGCCCCCGCGCGCGCGCGGCTCCTCCAGCGCTGCTGAGCGCATGCGCGCGAC 480  
Db 490 CGTTTCGCGCG-CCGAGGCGGTTTTTTTATAGGCGTTGTTGAGCGGTATGCGCGCGATT 433  
Qy 481 TTGAGAGCCCAAGCTGCTGCGCGCGCAGATCTGCTGAGCGTGTGCTGCTGCTGCTGCT 540  
Db 432 TTGAGGAGTTTACGTCGTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373  
Qy 541 GTGATCGTGTCCATGT 600

Db 372 GTGATCGGTGTTATGGTGGTGTGTTGCGTTAGTACGTTGTTGATTCGCGTACGTAAGTC 313  
Qy 601 GCCGACACCCGACCCCTGGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGGTGG 660  
Db 312 GTCGATATCGTAGTCTGTTGGTATGATCGGAGTAGGTATTTCGTCGGTTTGGGAGGAGTTT 253  
Qy 661 TTC 563  
Db 252 TTC 250  
XX  
XX RESULT 13  
XX ABQ49124/C  
XX ID ABQ49124 standard; DNA; 1634 BP.  
XX AC ABQ49124;  
XX DT 12-JUL-2002 (first entry)  
XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35715.  
XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
XX drug; side effect; cancer; central nervous system; cardiovascular;  
XX gastrointestinal; respiratory system; single nucleotide polymorphism;  
XX SNP; cell differentiation; ds.  
XX OS Homo sapiens.  
XX PN WO200218632-A2.  
XX PD 07-MAR-2002.  
XX PF 01-SEP-2001; 2001WO-EP01.0074.  
XX PR 01-SEP-2000; 2000DE-01043826.  
XX PR 05-SEP-2000; 2000DE-01044543.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX WPI; 2002-371829/40.  
XX  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
XX Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNPs); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
XX Sequence 1634 BP; 210 A; 232 C; 588 G; 604 T; 0 U; 0 Other;

Query Match 30.9%; Score 395.4; DB 6; Length 1634;  
 Best Local Similarity 78.8%; Pred. No. 7e-74;  
 Matches 497; Conservative 0; Mismatches 131; Indels 3; Gaps 2;

QY 1 ATGACCTTCGGGCGAGCGGGCGGCTCGGTGGTGTCTGAACGTGGGCGGCGCGGTAT 60  
 DB 909 ATAACCTTCGAACGCAACAAACGACCTCGAATACTAAACGTAACGACCGCGATAT 850

QY 61 TCGCTTCGCGGAGCTGTGAAGACTTCCCGCTCGCGGCTGAGCGGTGACACGCG 120  
 DB 849 TCGCTATCCGGAACACTTAAACACTTCCCGCTACGCGGTAAACGACTACACGAC 790

QY 121 TCGCGCTTCGAGGCGACGTGTGAGGTGTGCGAGGACTAGACGCGGAGGCGAACGAG 180  
 DB 789 TACCGCTTCGAACGCGACGTCTCGAATAATATACGAGCTAGACGCGGAACGCAACGAA 730

QY 181 TACTTCTTCGACCGGACCTCGAGGCGCTTCGCTCTCATCTCTCTACGTGCGGCGCAC 240  
 DB 729 TACTTCTTCGACCGGACCTCGAAGCTTCGACTCTCTCTCTCTCTCTCTCTCTCTCTCT 670

QY 241 GCGAAGCTGCGTTCGCGCGCGGATGTGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
 DB 669 GACAACTACGCTTCGCG-CGCGAATATACGAACCTCTCTCTCTCTCTCTCTCTCTCTCT 611

QY 301 TCGGGCTTCGAGGCGCGACCTCGAGTACTGCTGCGAGCGGCTCGACGCGCATG 360  
 DB 610 TAAACCTTAAACCGGACCTCGAATACTACTACCAACGCGCTCGACCGCGCAT 551

QY 361 TCGACACCTACACCTTCTACTCGGCGGACGCGGCGTCTGCGCGCGGCGGCGGCGGCGG 420  
 DB 550 TCGGACACCTACACCTTCTACTCGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGG 491

QY 421 CGCGCGGCGGCGGCGGCGGCTCGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 DB 490 CGCGCGGCGGCGG-CGAAACGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 433

QY 481 TTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
 DB 432 TTCGAAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 373

QY 541 GTGATGCTGTCATGCTGT 600  
 DB 372 GTAATGCTATCAT 313

QY 601 GCGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 631  
 DB 312 GCGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 282

RESULT 14  
 ID ABQ49125  
 AC ABQ49125;  
 XX  
 XX  
 DT 12-JUL-2002 (first entry)  
 XX  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35716.  
 XX  
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 XX drug; side effect; cancer; central nervous system; cardiovascular;  
 XX gastrointestinal; respiratory system; single nucleotide polymorphism;  
 XX SNP; cell differentiation; ds.  
 OS Homo sapiens.  
 XX  
 XX WC200218632-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 XX 01-SEP-2001; 2001WO-EP010074.  
 XX  
 XX 01-SEP-2000; 2000DE-01043826.  
 PR

05-SEP-2000; 2000DE-01044543.  
 (EPIG-) EPIGENOMICS AG.  
 Olek A, Piepenbrock C, Berlin K, Guetig D;  
 WPT; 2002-371829/40.  
 Determining the degree of cytosine methylation in genomic DNA, useful for  
 diagnosis and prognosis, comprises selective hybridization of amplicons  
 from chemically treated DNA.  
 Claim 12; 56pp + Sequence Listing; 56pp; German.  
 This invention describes a novel method for determining the degree of  
 methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 genomic sample of DNA. The sample is treated chemically to convert  
 cytosine (C) but not methylated C, to uracil, then part of the genomic  
 DNA that contains the target C is amplified to form a labeled amplicon.  
 The amplicon is hybridised to two classes, each with at least one member,  
 of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 degree of hybridisation to both classes is determined from the label on  
 the amplicon. From the ratio of labels hybridised to the two classes of  
 oligomers, the degree of methylation is calculated. The method is used:  
 (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 and of a wide range of diseases, e.g. cancer, disorders of the central  
 nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 particularly by detecting mutations or single nucleotide polymorphisms  
 (SNP's); and (ii) for differentiation of cell or tissue types and for  
 investigating cell differentiation. The method allows the methylation  
 status of many C residues to be determined simultaneously. ABQ13410-  
 ABQ54121 represent genomic DNA sequences used to illustrate the method  
 for determining the degree of cytosine methylation described in the  
 disclosure of the invention

Sequence 1634 BP; 604 A; 588 C; 232 G; 210 T; 0 U; 0 Other;  
 Query Match 30.9%; Score 395.4; DB 6; Length 1634;  
 Best Local Similarity 78.8%; Pred. No. 7e-74;  
 Matches 497; Conservative 0; Mismatches 131; Indels 3; Gaps 2;

QY 1 ATGACCTTCGGGCGGCGGCGGCGGCTCGGTGGTGTCTGAACGTGGGCGGCGCGGTAT 60  
 DB 726 ATAACCTTCGAACGCAACAAACGACCTCGAATACTATAACGTAACGCGCGGATAT 785

QY 61 TCGCTTCGCGGAGCTGTGAAGACTTCCCGCTCGCGGCTGAGCGGCTGACGCGGCG 120  
 DB 786 TCGCTATCCGGAACACTTAAACACTTCCCGCTACGCGCGGTAAACGACTACACGAC 845

QY 121 TCGCGCTTCGAGCGGCGGCGGCTCGAGGTGTGCGAGGACTACGACCGCGGCGGCGGAG 180  
 DB 846 TACCGCTTCGAGCGGCGGCGGCTCGAATAATATACGAGGACTACGACCGGCGGCGGAG 905

QY 181 TACTTCTTCGAGCGGCGGCGGCTCGGAGGCGGCTCGGCTTCTCTCTCTCTCTCTCTCTCT 240  
 DB 906 TACTTCTTCGAGCGGCGGCGGCTCGGAGGCGGCTCGGCTTCTCTCTCTCTCTCTCTCTCT 965

QY 241 GCGAAGCTGCGTTCGCGCGGCGGCGGCTGCGAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
 DB 966 GACAACTACGCTTCGCG-CGCGAATATACGACTCTCTCTCTCTCTCTCTCTCTCTCTCT 1024

QY 301 TGGGGCTTCGAGGCGGCGGCGGCGGCTCGAGTACTGTGCGAGGCGGCGGCTCTGACGCGG 360  
 DB 1025 TAAACCTTAAACCGGCGGCGGCTCGAATACTACTTACCAACGCGGCGGCTCTGACGCG 1084

QY 361 TCGGACACCTTACCTTCT 420  
 DB 1085 TCGGACACCTTACCTTCT 1144

QY 421 CGCGCGGCGGCGGCGGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
 DB 1145 CGCGCGGCGGCGG-CGAAACGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1202



QY 481 TTGAGGAGCCACGTCGTGCTGGCGGCGGAGATCCTGGCTAGCGTGTGGTGTTC 540  
 Db 1203 TTGGAARAAACCCACGTCGTGCTAACGGCGCAATCTTAACGATATCGATAATTC 1262  
 QY 541 GTGATCGTTCATGGTGTGCTGTGGCGGAGACAGCTTCCCGACTGGGCGCAACGAGCC 600  
 Db 1263 GTAATCGTATCCCAATAATACTACTATACGCAACACGTTACCCGACTAACGCAACCAACC 1322  
 QY 601 GCGGACAAACGCGAGCTGGATGACCGGAGCA 631  
 Db 1323 GCGGACAAACGCGAACCTAAATAACCGAARACA 1353

RESULT 15  
 ID ABK27494  
 ID ABK27494 standard; cDNA; 461 BP.  
 XX AC ABK27494;  
 XX DT 09-APR-2002 (first entry)  
 XX DE DNA encoding novel human ion channel protein #25.  
 XX KW Human; ion channel; anti-HIV; analgesic; cytostatic; antidiabetic;  
 KW anorectic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant;  
 KW antithrombotic; neuroleptic; antimigraine; antiparkinsonian;  
 KW tranquiliser; antidepressant; neuroprotective; anticonvulsant; pain;  
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
 KW antipsoriatic; antiaslathmatic; vulnarary; neurological disorder; obesity;  
 KW psychiatric disorder; gene therapy; asthma; traumatic brain injury;  
 KW human immunodeficiency virus; HIV-1; HIV-2; cancer; diabetes; anorexia;  
 KW myocardial infarction; Parkinson's disease; schizophrenia; anxiety;  
 KW dementia; Huntington's disease; thyroid disorder; inflammation;  
 KW autoimmune disorder; hormonal disorder; renal failure; psoriasis;  
 KW movement disorder; gene; ss.  
 OS Homo sapiens.

XX WO200185788-A2.  
 XX 15-NOV-2001.  
 XX 10-MAY-2001; 2001WO-US014965.  
 XX 10-MAY-2000; 2000US-0203305P.  
 XX 23-MAY-2000; 2000US-0206526P.  
 XX 25-MAY-2000; 2000US-0207033P.  
 XX 25-MAY-2000; 2000US-0207092P.  
 XX 25-MAY-2000; 2000US-0207093P.  
 XX 07-JUL-2000; 2000US-0216893P.  
 XX 04-AUG-2000; 2000US-0223245P.  
 XX 04-OCT-2000; 2000US-0237873P.  
 XX (PHAA ) PHARMACIA & UPJOHN CO.  
 XX Robertds SL, Benjamin CW, Karnovsky AM, Ruble CL;  
 XX WPI; 2002-062237/08.  
 XX P-PSDB; AAU81345.  
 XX New polynucleotied, useful for identifying ion channel activity  
 PT modulators that are used for treating Parkinson's disease, schizophrenia,  
 PT migraine, anxiety, manic depression, encodes the ion channel polypeptide.  
 XX Claim 1; Page 86; 172pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) which  
 CC encodes a novel ion channel protein, ion-x (II). The nucleic acid,  
 CC protein and antibody are useful for identifying a compound which binds a  
 CC nucleic acid molecule encoding ion-x. These are useful for treatment of a  
 CC neurological or psychiatric disorder which modulates ligand binding to  
 CC ion-x in neurons of the mammal; in gene therapy to restore ion-x activity  
 CC in certain disease states; for treating asthma, traumatic brain injury,

CC etc; modulators of ion-x activity or expression are useful for treating  
 CC diseases such as viral infections caused by human immunodeficiency virus  
 CC (HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,  
 CC hypotension, hypertension, thrombosis, myocardial infarction,  
 CC cardiomyopathies, atherosclerosis, Parkinson's disease, schizophrenia,  
 CC migraine, anxiety, manic depression, dementia, Huntington's disease,  
 CC thyroid disorders, inflammatory conditions, rheumatoid arthritis,  
 CC autoimmune disorders, hormonal disorders, renal failure, psoriasis, and  
 CC movement disorders. ABK27470-ABK27517 represent human ion channel protein  
 CC coding sequences and PCR primers of the invention  
 XX  
 SQ Sequence 461 BP; 109 A; 93 C; 98 G; 161 T; 0 U; 0 Other;

Query Match 30.0%; Score 383; DB 6; Length 461;  
 Best Local Similarity 99.7%; Pred. No. 2.3e-71;  
 Matches 394; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 885 CATTGGTCTTCAGACACTCGGTTTGACTCTCAAAACGTTGTACCGAG-AGATGGTTATGT 943  
 Db 1 CATTGGTCTTCAGACACTCGGTTTGACTCTCAAAACGTTGTACCGAGAGATGGTTATGT 60  
 QY 944 TACTTGTCTTCATTGTGTGTCCTATGCGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAAC 1003  
 Db 61 TACTTGTCTTCATTGTGTGTCCTATGCGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAAC 120  
 QY 1004 ATGGGCTGGACCTGGAAACATCCAAACGAGACTTTACCAAGCTTCTGCTGCTGCTGGT 1063  
 Db 121 ATGGGCTGGACCTGGAAACATCCAAACGAGACTTTACCAAGCTTCTGCTGCTGCTGGT 180  
 QY 1064 GGGTCATTATCTCTATGACTACAGTTGGCTATGGAGATATGTATCCTATCACAGTGCCTG 1123  
 Db 181 GGGTGATTATCTCTATGACTACAGTTGGCTATGGAGATATGTATCCTATCACAGTGCCTG 240  
 QY 1124 GAAGAATCTTGGAGAGTTGTGTTCTCAAGTGAATTTCTTATTGGCATTACCTATCA 1183  
 Db 241 GAAGAATCTTGGAGAGTTGTGTTCTCAAGTGAATTTCTTATTGGCATTACCTATCA 300  
 QY 1184 CTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGCTCAAGTTTATAGATCTGCTAGGT 1243  
 Db 301 CTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGCTCAAGTTTATAGATCTGCTAGGT 360  
 QY 1244 ATAGTAGAGCCTCTCCACTGAATTCCTGAATTA 1278  
 Db 361 ATAGTAGAGCCTCTCCACTGAATTCCTGAATTA 395

Search completed: October 6, 2004, 18:07:16  
 Job time : 590 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 17:08:52 ; Search time 114 Seconds  
(without alignments)  
6221.292 Million cell updates/sec

Title: US-10-016-647-1  
Perfect score: 1278  
Sequence: 1 atgaccttcggcgagcggg.....ccactgaattcctgaataa 1278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.4	21.7	2127	1 US-08-464-340A-1	Sequence 1, Appli
2	277.4	21.7	2127	5 PCT-US94-08449A-1	Sequence 1, Appli
3	258.8	20.3	2022	4 US-09-719-919A-18	Sequence 18, Appli
4	251	19.6	1518	4 US-09-719-919A-2	Sequence 2, Appli
5	198.2	15.5	2483	1 US-08-464-340A-3	Sequence 3, Appli
6	198.2	15.5	2483	5 PCT-US94-08449A-3	Sequence 3, Appli
7	197.8	15.5	3102	4 US-09-336-643A-17	Sequence 17, Appli
8	182.4	14.3	2494	4 US-09-181-339-6	Sequence 6, Appli
9	157.4	12.3	3080	4 US-09-336-643A-7	Sequence 7, Appli
10	146	11.4	2266	4 US-09-181-339-11	Sequence 11, Appli
11	146	11.4	2293	4 US-09-336-643A-5	Sequence 5, Appli
12	122	9.5	267	4 US-09-016-434-169	Sequence 169, App
13	115.4	9.0	1273	4 US-09-181-339-8	Sequence 8, Appli
14	113.4	8.9	1341	4 US-10-162-012-7	Sequence 7, Appli
15	107.8	8.4	2799	4 US-09-181-339-2	Sequence 2, Appli
16	100.6	7.9	1599	1 US-08-288-405A-9	Sequence 9, Appli
17	97.6	7.6	3424	4 US-09-336-643A-9	Sequence 9, Appli
18	95.4	7.5	696	1 US-07-955-916-5	Sequence 5, Appli
19	94.8	7.4	1994	1 US-08-527-152-1	Sequence 1, Appli
20	93.8	7.3	1805	1 US-07-955-916-6	Sequence 6, Appli
21	93	7.3	2064	4 US-09-178-109-3	Sequence 3, Appli
22	93	7.3	2072	4 US-09-142-791A-3	Sequence 3, Appli
23	93	7.3	2104	4 US-09-142-791A-1	Sequence 1, Appli
24	93	7.3	2121	4 US-09-178-109-1	Sequence 1, Appli
25	91.4	7.2	2104	4 US-09-142-791A-5	Sequence 5, Appli
26	88	6.9	774	4 US-09-181-339-4	Sequence 4, Appli
27	86.8	6.8	625	4 US-09-181-339-1	Sequence 1, Appli

28	80	6.3	1927	4	US-09-336-643A-3	Sequence 3, Appli
29	78.8	6.2	2118	4	US-09-016-434-1304	Sequence 1304, Ap
30	65.4	5.1	2787	3	US-09-105-537-40	Sequence 40, Appli
31	65.4	5.1	5970	3	US-09-320-878-21	Sequence 21, Appli
32	65.4	5.1	5970	4	US-09-141-908-11	Sequence 11, Appli
33	65.4	5.1	5970	4	US-09-657-440-21	Sequence 21, Appli
34	61.6	4.8	1812	4	US-09-252-991A-16103	Sequence 16103, A
35	61.6	4.8	1938	4	US-09-352-991A-16308	Sequence 16208, A
36	61.6	4.8	3744	4	US-09-352-991A-16389	Sequence 16389, A
37	61.4	4.8	241	4	US-09-016-434-779	Sequence 779, App
38	61	4.8	1777	1	US-08-173-508-5	Sequence 5, Appli
39	61	4.8	1777	2	US-08-365-310-5	Sequence 5, Appli
40	58.4	4.6	3074	4	US-08-951-742-5	Sequence 5, Appli
41	58.4	4.6	3137	4	US-09-813-148-1	Sequence 1, Appli
42	58.4	4.6	3137	4	US-08-590-304-1	Sequence 1, Appli
43	57.2	4.5	1119	4	US-09-252-991A-13578	Sequence 13578, A
44	57.2	4.5	2349	4	US-09-252-991A-13765	Sequence 13765, A
45	57.2	4.5	3081	4	US-09-252-991A-13660	Sequence 13660, A

ALIGNMENTS

RESULT 1  
US-08-464-340A-1  
; Sequence 1, Application US/08464340A  
; Patent No. 5710019  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,340A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: PCT/US94/08449  
FILING DATE: 28 JUL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-415  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2127 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: cDNA  
US-08-464-340A-1

Query Match 21.7%; Score 277.4; DB 1; Length 2127;  
Best Local Similarity 55.2%; Pred. No. 16-54;  
Matches 676; Conservative 0; Mismatches 501; Indels 48; Gaps 5;  
QY 38 TGAACGTGGCGCGCCCGTATTCGTCGCGGAGCTCTGAAGAGATTCCCGTGC 97  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db	481	TCAACGTAGGGCGCATCAAGTACTCGTGCCTCGCCTGGACCAACGCTGGACGAGATTCCCGCTGA	540
Qy	98	GC CGCGTGAAGCCGGCTGCACGGTTCGCGCTCCGAGCGCGACGTCCTCGAGAGTGTGGACG	157
Db	541	CGCGCTGGCCAGCTCAAGGCCTGCACCAACTTCGACGACATCCTCAACGTGTGGATG	600
Qy	158	ACTACGACCGGAGCGGAACGAGTACTTCTTCGACCGGCACTCGAGGCCCTTCGGCTTCA	217
Db	601	ACTACGACGTCACTGTCAACGAGTTCTTCTTCGACCGCAACCCGGGGCCCTTCGGCACTA	660
Qy	218	TCCTGTCTTACGTGCGGGCCACGCGAAGCTGCGCTTCGCGCCGCGGAGTGTGCGAGCTCT	277
Db	661	TCCTGACCTTCCTGGCGG---CGGGCAAGCTGCGGCTGCTCGCGAGATGTGCGCTGT	717
Qy	278	CCTTCTACAAACGAGATGATCTACTGGGGCTTGAGGGCGCGCACTTCGAGTACTGTGCC	337
Db	718	CCTTCCAGGAGGAGCTGCTACTTGGGGCATCGCGAGGACCACTCTGGACGGCTGTGCA	777
Qy	338	AGGCGCCCTCGACGACGCGATGCCACACCTACACTTCTACTCGCGCCGACGAGCGG	397
Db	778	AGCCCCCTACTCTCACAGAAGTTGAGAGATTGCGGAGATTGTGGACGCGGAGAGAGG	837
Qy	398	GC GTGTGGGCGCGACGAGCGCGCCCCGCGGGCCGAGGC-----GGCTCCCT	448
Db	838	ACGACGCGCTGGACAGCGAGAGGGCGCGACAGCAGAGGCGCGCGCGAGGGCGAGGGCGCC	897
Qy	449	CCAGGCGCTGGTAGAGCGCATCGGCGGACCTTCGAGGAGCCACCGTCTCTCGCTGCGCG	508
Db	898	TGGGGCCCTGCATGCGCGGCACTGCGCGACATGTTGGAGAGCGCGCACTCGGGGCTGCGTG	957
Qy	509	CGCAGATCTCGGCTAGCGGTTCGGTGCTGTTCGTGATCGTGTCCATGGTGGTCTCTGGCG	568
Db	958	GCAAGGTGTTGCGCTGCCCTGTCGTGCTCTTGTTGACCGTCAACGCGTCAACCTCTCCG	1017
Qy	569	CCAGCAGTTGCCGACATGGCGCAACCGACGCGCGCGACAAACCGAGCC-----TGGATG	622
Db	1018	TCAGCAGCTTGCCGAGCCTGAGGAGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1077
Qy	623	ACCGGACGAGATAAATTGAAGCTATCTGCATAGATTGGTTCACTGCCGAGTGATCGTGA	682
Db	1078	ACAACTCTTCACTGCTGAGTCCGTGTGCTGGCTGGTCTCCCTGGAGTTCCTCTCTGC	1137
Qy	683	GGTTCATTGCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAAATCATTTGATT	742
Db	1138	GGCTCATTCAGGGCCCCAGCAAGTTGCCCTTCCTCGGAGCCCGCTGACCTCATCGAAC	1197
Qy	743	TACTGGCAATCAGCCGATTAATACATCTCTGTGTTGATGACAGTGTTTACAGGCGAG---	798
Db	1198	TGTTGGCATCTGCCCCCTACTACATCAGCTGCTGTGTGGACGGCGCGCGCAGGCGGCTC	1257
Qy	799	-----AACTCTCAACTCAGAGGGCTGGAGTCACTTCAGGGTACTTA	841
Db	1258	GCAAGCCGCGCGGGCAACAGCTACTCTGCACAAAGTGGGGCTGGTCTCGCGGTGCTGC	1317
Qy	842	GAATGATGAGGATTTTGGGTGATTAAGCTTCCCGTCACTTCATGTGCTTCAGACAC	901
Db	1318	GGGCGCTGCGCATCCTGTACTGTATGCGCTTGGCGGCCACTCCCTGGGGCTCGACAGCG	1377
Qy	902	TCGGTTTGACTCTCAAAAGTTGCTACCGAGAGATGGTTATGTTACTTTGCTTCATTGTG	961
Db	1378	TGGGGCTCAGGCCCGCGCTGCACCCGCGAGTTTCGGGCTCCGTGCTCTTCTCTGCG	1437
Qy	962	TTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAAA	1021
Db	1438	TGGCCATCGCCCTCTCGCCCCCTGCTACGTCATCGAAGACGAGATG-----1488	
Qy	1022	CATCCAAACAAGGACTTTACAGAGATTCCTGTGCTCTCGTGGTGGGATTAATCTCTATGA	1081
Db	1489	CCGACAGCCCCAGTTCAACGAGCATCCCTGCCTCTACTGTTGGGCTGTCAACCATGA	1548
Qy	1082	CTACAGTTGCTATGGAGATATGATTCCTATCACAGTGCCTGGAAAGTAATCTTTGGAGGAG	1141
Db	1549	CGACGTTGACATATGGCGCATGTGTCCCAAGAGACACCCGGGCGAGGTAGTGCCTCTGA	1608

QY 1142 TTGTGTTGTCAGTGAATTGTTCTATTGCATTACCTATCACTTTTATCTACCATAGCT 1200  
 Db 1609 GCAGCATCCTGAGCGGCATCCTCTCATGGCCTTCCAGTCACCTCATCTTCCACACCT  
 QY 1202 TTGTGCAGTGTATTATCATGAGCTCAA 1226  
 Db 1669 TCTCCCCCTCTTACCTGGAGCTCAA 1693  
 RESULT 2  
 PCT-US94-08449A-1  
 ; Sequence 1, Application PC/TUS9408449A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LI, ET AL.  
 ; TITLE OF INVENTION: Potassium Channel Protein 1 and 2  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 ; STREET: 6 BECKER FARM ROAD  
 ; CITY: ROSELAND  
 ; STATE: NEW JERSEY  
 ; COUNTRY: USA  
 ; ZIP: 07068  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 INCH DISKETTE  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WORD PERFECT 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/08449A  
 ; FILING DATE: SUBMITTED HERewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FERRARO, GREGORY D.  
 ; REGISTRATION NUMBER: 36,134  
 ; REFERENCE/DOCKET NUMBER: 325800-105  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-994-1700  
 ; TELEFAX: 201-994-1744  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2127 BASE PAIRS  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: SINGLE  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: CDNA  
 PCT-US94-08449A-1

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QY 278 CTTTCTAACACGAGATGATCTACTGGGCTTGGAGGGCGCGCACTCGAGTACTCTCTGCC 337
Db 718 CTTTCCAGAGAGAGTGTGTACTGGGCTTGGAGGGCGCGCACTCGAGTACTCTCTGCC 777
QY 338 AGCGCGCTTCCAGACCGCATGTCCGACACCTACACCTTCTACTCGCGCGAGAGCGG 397
Db 778 AGCGCGCTTCTCGAAGATTTAGAGTTTCCGAGATGTTGGAGCGGAGGAGAGG 837
QY 398 GCGTGTCTGGCGCGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448
Db 838 AGCAGCGCTTCCAGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897
QY 449 CCAGCGCTTGGCGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 508
Db 898 TGGCGCGCTTGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 957
QY 509 CGCAGATCTTGGCTAGCGTGTGGTGTGTCTGATCGTGTCTTCCATGTGTGTGTGTGCG 568
Db 958 GCAAGGTGTTCGCTGCTGTGGTGTCTTCTGTCACCGTCAACCGCTCAACCTCTCGG 1017
QY 569 CCAGCAGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 622
Db 1018 TCAGCAGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1077
QY 623 ACCGAGCAGGATAATTGAAGTATCTGCATAGGTTGGTTCATCTCGCGAGTGCATCTGTA 682
Db 1078 ACAACGTCTTATCGTGGAGTGGTGTGGTGGGCTGGTTCCTCTGGAGTTCCTCTGCG 1137
QY 683 GGTTCATGTCTCCAAAACAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 742
Db 1138 GGCTCATTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1197
QY 743 TACTGGCAATACGCGCGTATTAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 798
Db 1198 TGGTGGCAATCTGCGCTTACTACTACATCAAGCTCTGTGTGTGTGTGTGTGTGTGTGT 1257
QY 799 -----AACTCTCAACTCCAGAGGCTTGGAGTCACTTGGAGGTAATTA 841
Db 1258 GCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1317
QY 842 GAATGATGAGATTTTGGGTGATTAAGCTTGGCGGTCACTTCAATGGTCTTCAAGAC 901
Db 1318 GGGCGCTGCGCATCTGTACGATGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1377
QY 902 TCGGTTTGACTCTCAACGTTCTACCGAGAGATGTTATGTATGTCTTCTTCAATTTGT 961
Db 1378 TGGGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1437
QY 962 TTGGCATGGCAATCTTTAGTGACATTTCTCAGCTTCTTGAACATGGGTGGACCTGGAAA 1021
Db 1438 TGGCCATCGCCCTCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1488
QY 1022 CATCAACAAGAGACTTTACAGCATTTCTGTCTGTCTGTGGTGGTGGTATCTCTATGA 1081
Db 1489 CCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1548
QY 1082 CTACAGTGGCTATGAGATATGTAATCTATACAGTGCCTGGAGAAATTTCTTGAGAG 1141
Db 1549 CGACGCTGAGCTATGGCGACATGGTCCCGAGAGCACCGCGCGCGCGCGCGCGCGCGCG 1608
QY 1142 TTTGTGTTGTGAGTGAATTTCTATTGGCATTTACCTATCACTTTTATCTACCATAGCT 1201
Db 1609 GGAGCATCTGAGCGCATCTTCTGCTCATGGCGCTTCCAGTCACTCCATCTTCCACACT 1668
QY 1202 TTGTGCGAGTGTATCATGAGCTCAA 1226
Db 1669 TCTCCCGCTCTTACCTGGAGCTCAA 1693
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## RESULT 3

US-09-719-919A-18

; Sequence 18, Application US/09719919A

; Patent No. 6680180

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; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN Incorporated
; TITLE OF INVENTION: Kv6.2, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001410US
; CURRENT APPLICATION NUMBER: US/09/719,919A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/091,466
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/14945
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (149)..(1708)
; OTHER INFORMATION: human alpha subunit of heteromeric voltage-gated
; OTHER INFORMATION: potassium channel Kv6.2
; US-09-719-919A-18
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Query Match 20.3%; Score 258.6; DB 4; Length 2022;
Best Local Similarity 54.1%; Pred. No. 2.9e-50;
Matches 664; Conservative 0; Mismatches 522; Indels 42; Gaps 5;

QY 30 GGTGGTCTGAAGCTGGCGCGCGCGGTATTCGCTGTCCCGGAGCTGTGAAGACTT 89
Db 328 GATCCTGATCAACGTGGGGGCGAGAGGTATCTCTCCCTGGAGCACACTGACCGGTT 387
QY 90 CCGCTCGCGCGGTGAGCGCGCTGCACGCTCCGCTCGAGCGGCGGACGTCTCGAGGT 149
Db 388 CCGCTGAGCGCGCTGAGCAAACTCAGGCTCTGTGGAGCTACAGAGATCTGCGAGCT 447
QY 150 GTGCGAGCTACGACCGCGAGCGCAACGAGTACTTTCGACCGGCACTTCGAGGCGCTT 209
Db 448 CTGCGATGATTACGACGAGGACAGCCAGGAGTTCTTCTTCGACAGGAGCCAGCGCCTT 507
QY 210 CGGCTTCATCTGCTCTACGTGGCGCGCGCGAGCTCGCTTCGCGCGCGGATGTG 269
Db 508 CGGCGTGTATCGTGGCTTCTG---GGCGCGGGAAGCTGGTCTTCTGAGGAGATGTG 564
QY 270 CGAGCTCTCTTTACAAAGAGATGATCTACTGGGGCTGGAGGGCGCGCACCTCGAGTA 329
Db 565 CGCGCTCTCTTCAGAGAGAGCTGGCTTACTGGGCGATCGAGGAGGCCCACTTGGAGAG 624
QY 330 CTGTGCGCGCGCGCTTCGACGACCGCATGTCCGACACCTACACCTTCTACTCGGCGGA 389
Db 625 GTGTGCTTCGGAAGCTGTGAGAGCTGAGAGAGCTGAGAGAGCTGGAGAGCTGCCAAGTGA 684
QY 390 CGAGCGCGCGGTGTGGCGCGCA---CGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 446
Db 685 CAGGAGAGCTACTGAGGCGAGCAGAGGAGAGCCCGCGCGCGCGCTTCGACCTCTCGCG 744
QY 447 CTCAGCGCGTGTGTGAGCGCATGCGGCGGACCTTGGAGAGCGCCACGTCGTGTGTGCG 506
Db 745 CTGGGCGCTGTGATGAACCGGCTGCGGAGATGTTGGAAGAACCCGAGTCCGGGCTGCC 804
QY 507 GCGCGAGATCTCGGTAGCTGTGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 566
Db 805 CGGAAGAGTCTTGGCTTGGCTTCTCCATCTCTTCTGGGCGCCACAGAGCGCTCAGCCTGTG 864
QY 567 CGCGAGCAGCTTGGCGGAGCTGGGCG-----AAGCAGCGCGCGCGCAACCGCAGCCTGGA 620
Db 865 TGTCAGCACCATGCCCGACCTCAGGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 924
QY 621 TGACCGGAGCAGGATTAATGAAGCTATCTCATAGTGGTGTGGTGTGGTGTGGTGTGGTGT 680
Db 925 CTACTATATTTTATCGTGGAGACCATCTGCGTGGCGCTGGTCTCTCCCTGTGGCTTGCCT 984
QY 681 GAGGTTTCAATGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGAGCCCCCTGAAACATCATTA 740
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Db 1253 GCTATGGGACATGGTCCCTCGCAGCGTCCGGGACAGATGGTGGCTCTGAGCAGCATCC 1312  
QY 1151 TCAGTGGAAATGTTCTATTTGGATTACCTATACATTTTATCTACATAGCTTTGTGAGT 1210  
Db 1313 TTAGCGGATCCTTATCATGGCTTTCCAGCCACATCATCTTCCACACGTTCTCTACT 1372  
QY 1211 GTTATCATGAGCTCAAG 1227  
Db 1373 CCTACTGGAGCTGAAG 1389

## RESULT 5

US-08-464-340A-3  
; Sequence 3, Application US/08464340A  
; Patent No. 5710019  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESS: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,340A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08449  
; FILING DATE: 28 JUL 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2483 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: CDNA

US-08-464-340A-3  
Query Match 15.5%; Score 198.2; DB 1; Length 2483;  
Best Local Similarity 50.9%; Pred. No. 2,5e-36;  
Matches 625; Conservative 0; Mismatches 568; Indels 36; Gaps 5;  
QY 3 GACCTTCGGGCGAGCGGGCGGCTCGGTGTGTGAACGTGGCGGCGCGCGGTATTC 62  
Db 729 GAGCTCCGCTGCGAGCGGACATAGATAGTCTCAACGTGGGGGGCGTGGCGCAGT 788  
QY 63 GCTGTCCCGGAGCTGCTGAAGACTTCCGCTGCGCGCGGTGAGCCGCGTGCACGGGTG 122  
Db 789 GCTGTACGGGGACCTCCTCAGTCAGTACCTGAGACCGCGCTGGCGAGCTCATCAATG 848  
QY 123 CGGCTCCGAGCGGAGCG-----TGCTCGAGGTGTGCGAGCTACGACCGCGGCGCAA 176  
Db 849 CTTGGCTGGGGGTACGACACCATCTTCTCCCTGTGGAGCAGTACGACCGCGGCAAGCG 908  
QY 177 CGAGTACTTCTTCGACCGGCACTCGAGAGCGCTTCGGCTTCATCTCTAGCTGGCGG 236

Db 909 CGAGTTCTACTTTTGCAGGAGCAGCGGCTTCAAGTGTGTC---ATCGAGGTGACTA 965  
QY 237 CCGCGGCAAGCTCGGCTTCGCGCGGAGTGTGCGAGCTCTCCTTCTACAAACAGATGAT 296  
Db 966 TTTGGGGAGGTCCACATGAAGAGGCATCTGCCCATCTGCTTCAAGAACAGATGGA 1025  
QY 297 CTACTGGGGCTGGAGGGCGGCACCTCGAGTACTGCTGCAGCGCGGCTCGACGACCG 356  
Db 1026 CTTCTGAAGTGGACCTCAAGTTCTTGAGCAGTGTGTGAAGAGCCACC----- 1075  
QY 357 CATGTCGACACCTACACCTTCTACTCGCCGAGAGCGGGGCTGCTGGCGCGGACGA 416  
Db 1076 --TGAGCGAGAGCGGAGAGTGGAGGAGATCGCGCGCGCTGAGCTCATCTGGA 1133  
QY 417 GGCGCGCGCGCGGCGCGGAGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGGCGCG 476  
Db 1134 CGACCTGGGCTGGACGCGCGCGGCGGCTGGCGCGCTGCAGAAAGTGTGCTGAA 1193  
QY 477 GACCTTCGAGAGCGGAGTGTGCTGGCGCGGAGATCCTGCTAGCGTGTGGTGGT 536  
Db 1194 GTTCTCGAGAGCGGAGTGTGCTGGCGCGGCGGCTGGCGGCTGCTCTCTCTCT 1253  
QY 537 GTTCTGATCGTGTCCATGCTGTGCTGCGCGCAGCAGCTTCCCGACTGGCGCAACGC 596  
Db 1254 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313  
QY 597 AGCGCGGACAAACCGGAGCTGGATGACCGGA---GCAGGATATTAAGACTATCTGCAT 653  
Db 1314 GGACGCGGAGGCAACCGCGTGGAGCACCAGCGCTGGAGAGCTGGAGAGCGGCTGCAT 1373  
QY 654 AGTTGGTTTCACTGCGAGTGCATCGTGAGTTTCATTGTCTCCAAAACAAAGTGTGAGTT 713  
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QY 714 TGTCAAGAGACCCCTGAACATCATTTGATTTACTGGCAATCACGCGTATTTACATCTCTGT 773  
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QY 774 GTTATGACAGTGTTTACAGCGGAGACTCTCACTCCAGAGGCTGGAGTCACTTTGAG 833  
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Db 1614 CGAGACCTCACCTATGCTTCAAGCGCAGCTTCAAGGAACTGGGGCTGCTGCTCATGTA 1673  
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Db 1674 CTTGGCAGTGGTATCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1721  
QY 1014 CTTGGAACATCCAAAGGAGCTTTACAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073  
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QY 1074 CTCTATGACTACAGTGGCTATGAGATATGATCTCTATCAGAGTGGCTGAGAAATCT 1133  
Db 1782 CACCATGACCAACCGTGGCTACGCGGACATCTACCCCAAGACACGCTGAGCAGCTCAA 1841  
QY 1134 TGGAGGAGTTGTCTGCTGAGTGAATTTGTTTATTGGCATTACCTATCATCTTTTATCTA 1193  
Db 1842 CGCGCCCATCAGCTTCTTGTGTGTGTGTCATTGCCATCGCGCTGCCCATCCACCCCATCAT 1901  
QY 1194 CCATAGCTTTGTGAGTGTGTTATCATGAGC 1222  
Db 1902 CAACAACCTTTGTCAGGTACTACACAAGC 1930

## RESULT 6

PCT-US94-08449A-3

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; Sequence 3, Application PC/TUS9408449A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1 and 2
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449A
; FILING DATE: SUBMITTED HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; PCT-US94-08449A-3

Query Match 15.5%; Score 198.2; DB 5; Length 2483;
Best Local Similarity 50.9%; Pred. No. 2.5e-36;
Matches 625; Conservative 0; Mismatches 568; Indels 36; Gaps 5;

QY 3 GACCTTCGGCGCAGCGCGCGCTCGGTGGTGTGAACGCTGGCGCGCGCGCTATTC 62
DB 729 GAGCTCGCTGCCAGCGACGACATAGATAGTCTCAACGCTGGGGGGCTCGGCAGGT 788
QY 63 GCTGTCGGCGAGCTGCTGAAGGACTTCCCGCTGCGCGCGCGCTGAGCGCGCTGCA 122
DB 789 GCTGTACGGGAGCTCTCAGTCAGTACCTGAGACCGCGCTGGCGAGCTCATCAACTG 848
QY 123 CCCTCCGAGCGGAGC-----TGCTCGAGGTGTCGACGACTAGACCGGAGCGCAA 176
DB 849 CTTGGCTGGGGGTACGACACCACTCTCCCTGTCGACGACTAGACCGCGGAGGG 908
QY 177 CGAGTACTTCTTCGACCGGACCTCGGAGCGCTTCGCGCTTCATCTGCTCTACGAGATGAT 236
DB 909 CGAGTCTACTTTGACAGGAGCGCGGACGCTTCAAGTGTGTC---ATCGAGGTGACTA 965
QY 237 CCACGGCAAGCTGCGCTTCGCGCGCGGATGTCGAGCTCTCTCTTCTACAGGATGAT 296
DB 966 TTTCTGGAAGTGGACCTCAAGTTCTCTGGACGACTGTTCCAGAGCCACC----- 1075
QY 297 CTACTGGGCGCTGGAGGGCGCGCACCTCGAGTACTGCTGCCAGCGCGCTCGACGCG 356
DB 1026 CTTCTGGAAGTGGACCTCAAGTTCTCTGGACGACTGTTCCAGAGCCACC----- 1075
QY 357 CATGTCGACACCTACACTTCTACTCGGCGGACGAGCGCGGCTGCTGGCGGCGGAGA 416
DB 1076 --TGACGGAAGCGCGGAGGAGCTGGAGGAGATCGCGCGCGCGCTCATCTCTGGA 1133

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RESULT 7  
 US-09-336-643A-17  
 ; Sequence 17, Application US/09336643A  
 ; Patent No. 6399761  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miller, Andrew P.  
 ; APPLICANT: Curran, Mark Edward  
 ; APPLICANT: Hu, Ping  
 ; APPLICANT: Rutter, Marc  
 ; APPLICANT: Wang, Jian-Wang  
 ; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
 ; FILE REFERENCE: SEQ-15P  
 ; CURRENT APPLICATION NUMBER: US/09/336,643A  
 ; FILING DATE: 1999-06-18  
 ; PRIOR APPLICATION NUMBER: 60/076,667  
 ; PRIOR FILING DATE: 1998-08-07

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QY 417 GGCGCGCGCGCGCGCGCGCGCTCCCTCAGAGCGCTGCTGGAGCGCATGCGGCG 476
DB 1134 CGACCTGGCGGTGGACGCGCGCGCGCGCTGGCGCGCGCTGGCGCGCATGGAA 1193
QY 477 GACCTTCGAGGAGCCACGCTGCTGGCGCGCGCGCATCTGGCTAGCGTGTGGTGT 536
DB 1194 GTTCTGAGAGAGCCGAGTGTGCTGGCGCGCGCGGTGGTGGCGAGCTCTCTCT 1253
QY 537 GTTCTGATCGTGTCCATGTGTGCTGGCGCGCGCATCTGCCGAGCTGGCGCAAC 596
DB 1254 GCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313
QY 597 AGCGCGCGCGCGCGCGCGCGCTGGATGACCGGA---GCAGGATAATTGAAGCTATCTG 653
DB 1314 GGACCGCGCGCGCGCGCGCGCTGGAGCACCGCGCTGGAGAGAGCTGGAGAGCGG 1373
QY 654 AGGTGGTTTCACTGCCGAGTGCATCGTGGTTCATGTCTCCAAAACAAAGTGTG 713
DB 1374 TGGCTGGTTTCACTGCCGAGTGCATCGTGGTTCATGTCTCCAAAACAAAGTGTG 1433
QY 714 TGTCAAGAGAGCGCGCGCGCGCTGATGATGATGATGATGATGATGATGATGAT 773
DB 1434 CGCGCTGCTCTTCAATGAACATGTTGGAGCTGCTGGCGCATCTCTCTCTTCT 1493
QY 774 GTTGATGACAGTGTGTTTACAGCGCGAGAACTCTCAACTCCAGAGCGCTGGAGT 833
DB 1494 CACGCTCAGCGCGCGCGCGCGCGCTGATGATGATGATGATGATGATGATGATG 1553
QY 834 GGTACTTAGAATGATGAGGATGATGATGATGATGATGATGATGATGATGATGAT 893
DB 1554 GCGCTGCGGATCATGCGCATCGCGCATCTTCAAGCTGGCGCGCGCATCTCTCT 1613
QY 894 TCAGACACTCGGTTTGTACTCTCAAACTGCTCAAGAGAGATGTTATGTTATGTT 953
DB 1614 GCAGACCTTCACTATGCTTCAAGCGAGCTTCAAGAGCTGGGCTGCTGCTCAT 1673
QY 954 CATTTGTTGCCATGGCAATCTTTAGTGCATCTTTCAGCTCTTTCAGCATGGGCT 1013
DB 1674 CTTGGCAGTGGTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1721
QY 1014 CTTGAAACATCCAAACAGGACTTTTACAGCATCTTCTGCTGCTGCTGCTGCTG 1073
DB 1722 GCAGAGCATCCAGAGACCTGTTTAAAGACATCCCGAGCTCTTCTGGTGGCG 1781
QY 1074 CTCTATGACTACAGTGTGGCTATGGAGATATGATCTCTATCAGAGTGCCTGGA 1133
DB 1782 CACCATGACCGCTGCGCTACGCGGACATCTACCGAGACCGAGCTGAGCAAGCT 1841
QY 1134 TGGAGGAGTGTGTTGTTGCTGAGTGAATGTTCTATTGGCATTTACCTATCAT 1193
DB 1842 CGCGGCGCATGAGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1901
QY 1194 CCATAGCTTTTGTGAGTGTGTTATCATGAGC 1222
DB 1902 CAACAACTTTGTGAGTGTGTTATCAACAGC 1930

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; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274)...(1705)
; OTHER INFORMATION: K+Hnov11
US-09-336-643A-17

Query Match      15.5%; Score 197.8; DB 4; Length 3102;
Best Local Similarity 50.8%; Pred. No. 3.3e-36;
Matches 614; Conservative 0; Mismatches 547; Indels 48; Gaps 4;

QY 38 TGAAGTGGGGCGCGCGGTATTGCTGTCGCCGGAGCTGCTGAAGACTTCCGGCTGC 97
DB 335 TCAATGTGGCGGCTTCAAGAGAGCTGCGCTCGCACACGCTGCTGCGCTTCCCGGAGA 394
QY 98 GCCGGTGTAGCGGCTGCAAGCGCTCCGCTCCGAGCGCAGCTGCTCGAGGTGTGCGACG 157
DB 395 CGCGCTGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 454
QY 158 ACTAGACCGCGAGCGCAAGCTACTTCTTTCGACGGGCACTCGAGGCTTTCGCTTCA 217
DB 455 ACTAGACCGCGAGCGCAAGCTACTTCTTTCGACGGGCACTCGAGGCTTTCGCTTCA 514
QY 218 TCTGCTGTCTACGTGGCGGCCCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 277
DB 515 TGTGCTGCTTCTATC---ACACGGCAAGCTTTCAGTCTGAGCTGAGTGTGCTTCT 571
QY 278 CTTCTTCAACAGATGATCTACTGGGCTGGAGGGCGGCACTCGAGTACTGCTGCC 337
DB 572 CTTTCAAGCAGAGATCGAGTACTGGGCACTCAACAGGTTTCTTCACTGCTGCTGCTG 631
QY 338 AGCGCGCTGCTGACGACCGCATGTCCGACACCTTACCTTCTGCTGCTGCTGCTGCTGCT 397
DB 632 GTTACAGTACCATGGCGCAAGTAGAGCCCGAGCAGGAGAGTGGAGCAGCAGAGTG 691
QY 398 GGGTGTGGCGCGCG-----ACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 430
DB 692 ACCAGGAGAGCACCAGCTTCTTCTGATGATGCTTGGCTTCTTACACGAGCGCTCCA 751
QY 431 GGGCGGAGCGGCTCCCTCAGCGCTGCTGCGGCGATGCGCGGACCTTCGAGGAGC 490
DB 752 AGTTCGATGGGAGCGCGCTCGGCACTTCCGAGGAGCTGTGGCTGGCGCTGGACACC 811
QY 491 CCACGTGCTGCTGGCGCGCAGATCCTGGCTAGCGGTGTGCTGCTGCTGCTGCTGCTGCTG 550
DB 812 CCGGCTACTCAGTGTGAGCAGGGTCTTCAGCATCCTGTCCATCCTGTGTGTGATGGGT 871
QY 551 CCATGCTGTGTGTGCGGCGACAGCTTCCCGGCTGGGCGGCAACGAGCGCGC---GACA 607
DB 872 CCATCATCACCATGTGCTCAATAGCTGCTGCGCGATTTCCAAATCCCTGACAGCGGCA 931
QY 608 ACCGAGCGCTGATGACCGGAGCAGATAAATGAAGCTATCTGCAATAGTGTGTTCACTG 667
DB 932 ACCCTGGCGAGACCTTAGTTCGAATCGTGGAGCATTTGGCATTCGCTGTTTCAAT 991
QY 668 CCGAGTGCATCGTGAAGTTTATGTCTCCAAAAAAGAGTGTGAGTTGTCAAGACGCC 727
DB 992 TTGAGCTGTGGCGAGTTTGTGTGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1051
QY 728 TGAACATCATTTACTTACGGCAATCACGCGCTTATACATCTGCTGTTGTGATGACAGT 787
DB 1052 TAAACCTTATTGACCTCATGTCATGCTCCCTTTTACATCATCTGCTGTTGTGTAACCTGG 1111
QY 788 TTACAGGCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGAGGTACTTAGATGA 847
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DB 1112 TGGTGGAGAGCACACCTACTTTAGCCAACTTGGCAGGGTGGCCAGGTCTTGAGGCTGA 1171
QY 848 TGAGGATTTTTGGGTGATTAAAGCTTCCCGTCACTTCATTTGTTTCAGACACTCGGTT 907
DB 1172 TCGGATCTTCCGCACTCTTAAAGCTGGCCAGGCACTCCACTGGCTCCGCTCCGCTGGGG 1231
QY 908 TGACTCTCAACGTTGCTTACCGAGAGATGTTATGTTACTTGTCTTCAATTTGTTGCCA 967
DB 1232 CCACCTTTGAAATACAGCTACAAGAGTAGGGTGTCTTGTCTTACTCTCCGTGGGGA 1291
QY 968 TGGCAATCTTTTAGTGACATTTTCTCAGCTTTTGAACATGGGCTGGACCTGGAAACATCCA 1027
DB 1292 TTTCCATCTTCTCGTGGTGGCTTACACCATTTGAAAGAGGAGG-----A 1336
QY 1028 ACAAGGCTTTTACCAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
DB 1337 ACGAGGCGCTTGGCCACCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1396
QY 1088 TTGCTATGAGATATATATCTCTATCACAGTGTCTGGAAGAAATTTTGGAGGAGTTTGTG 1147
DB 1397 TGGGTACGGGATGTGTTCCAGGACACGCGAGGAAAGTGAAGTCTGCTGCTGCTGCTGCT 1456
QY 1148 TTGTCAGTGAATTTGTTCTATTTGTCATTAACATTAATTTTATCTTATCTTATCTTATCT 1207
DB 1457 TCTTGGCAGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1516
QY 1208 AGTGTATC 1216
DB 1517 ACTTTTACC 1525

RESULT 8
US-09-181-339-6
; Sequence 6, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033.30
; CURRENT APPLICATION NUMBER: US/09/181,339
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (449)...(1924)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2494)
; OTHER INFORMATION: n = A,T,C or G
US-09-181-339-6

Query Match      14.3%; Score 182.4; DB 4; Length 2494;
Best Local Similarity 49.9%; Pred. No. 1e-32;
Matches 607; Conservative 0; Mismatches 561; Indels 48; Gaps 4;

QY 38 TGAACGTGGGGCGCGCGGTATTGCTGTCGCCGGAGCTGCTGAAGACTTCCCGCTGC 97
DB 504 TGAACGTGGGGCGCGCGGTATTGCTGTCGATCAAAAGTACACTCTCTCGGTTCCTCACA 563
QY 98 GCCCGGTAGCGGCTGACGCGCTGCGCTCCGAGCGGCGCTGCTGAGGTGTGCGACG 157
DB 564 CACGACTGGGAAAGCTGCTTACCTGCGCACTCTGAGGAGGCCAATCTCGAGCTGTGTGATG 623
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QY 606 CAACCCGAGCCTGGATGACCGGAGCAGGATAATTAAGCTATCTGCATAGGTGGTTTCAC 665
Db 1181 AAGCTGGCTGGACCTCAGCTGCTGGAATCTGGAGTATGTGTGCAATAGCTGGTTTAC 1240
QY 666 TGCCGAGTGCATCGTGGGTTCAATCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACC 725
Db 1241 CGGGGAGTTTGTCTCGGTTCTGTGTGTGGGACAGGTGTGCTTCTTAAGAAAGT 1300
QY 726 CTGGAACATCATTAATTAATGATGCAATACCGCGTATTAATCACTCTGTGTGATGACAGT 785
Db 1301 GCCAAACATCATAGACCTCTGCTGCCATCTTGCCCTTCTACATCACTCTCTGATAGAG 1360
QY 786 GTTACAGCGGAGAACTC-----TCAAATCCAGAGGCTGGAGTCACTTGAGGGTACT 839
Db 1361 CCTAAGTGGAGCCAGACCGAGAGCTGGAGAACGTGGGGCGCATTTCCAGGTGTT 1420
QY 840 TAGAATGATCAGGAAATTTTGGGTGATTAAGCTTGCCCGTCACTTCATTGGTCTTCAGAC 899
Db 1421 GAGGCTGCTCAGGCTCTGGCATGCTAAAGCTGGGACAGATTCACAGGATTACGCTC 1480
QY 900 ACTCGGTTGACTCTCAAGCTGTACCGAGAGATGTTATGTTACTTGTCTTCAATTG 959
Db 1481 CCTTGGGATGACAAATCACCAGGTTTACGAAGAAGTCGGCTACTGCTCTATTTCTATC 1540
QY 960 TGTGTCATGGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAACTGGGCTGGACCTGGA 1019
Db 1541 CGTGGAACTCTATATTTTCACTGTAGATACATTGCTGAGCAAGCAATTC----- 1593
QY 1020 AACATCCAAACAGGACTTTACAGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
Db 1594 -----CTGACACAACTTCCAAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1648
QY 1080 GACTACAGTTGGCTATGGAGATGATGATCTATCAGTGTCTGGAAGAAATCTTGGAGG 1139
Db 1649 GACTACTGAGGATATGGGACATTAAGACAGACACACACAGGAAATCTGTCGCTT 1708
QY 1140 AGTTGTGTGTCAGGGAATGTTCTATTGCAATPACCTATCACTTTTATCTACCATAG 1199
Db 1709 CATGTATATATATCGGGAATCTTGTCTGCGCTTGCCTATTGCTATTATTAACGATCG 1768
QY 1200 CTT 1202
Db 1769 CTT 1771

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RESULT 10
US-09-181-339-11
; Sequence 11, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033.30
; CURRENT APPLICATION NUMBER: US/09/181,339
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2266
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (308)....(1783)
US-09-181-339-11

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Query Match 11.4%; Score 146; DB 4; Length 2266;  
 Best Local Similarity 48.0%; Pred. No. 2.3e-24;

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Matches 585; Conservative 0; Mismatches 585; Indels 48; Gaps 4;
QY 37 CTGAACGTGGCGCGCGCGGTATTCGTGTCTCCGGAGCTGCTGAAGGACTTCCCGCTG 96
Db 362 CTGAATGTGGGGGCTTTAGCAGTCTGTGACCAAGACCCCTCTCGCGTTTCTCAC 421
QY 97 CGCCGCTGAGCCCGCTGCACCGGTGCGCTCCGAGCGGACGCTGCTGAGGTGGGAC 156
Db 422 ACCAGACTGGGGAAGCTGCTTACTTGCATTTCTGAAGAGGCCAATCTGGAGCTGTGAT 481
QY 157 GACTACGACCGGAGCGCAACGAGTACTTCTTCCACCGGCACTCGAGGCGCTTCGGCTTC 216
Db 482 GATTACAGTGTGGCGATAGGAATACTACTTTGATCGGAATCCCTCTTCTTTCAGATAT 541
QY 217 ATCTGCTGTACGTGTGGCGGCCACGGCAAGTGTGGCTTTCGGCCGCGGATGTGAGGCTC 276
Db 542 GTTTTGAATT---TTTATTACACGGGGAAGTGTGATCTCATGGAGGAGCTGTGCGTATTC 598
QY 277 TCCCTTCTACACAGATGATCTACTGGGCTGTGAGGCGCGGACCTCTGAGTACTGCTGC 336
Db 599 TCATCTGCGAGGAGATCGAGTACTGGGCAATCAAGAGCTCTCATGATTTCTTGTGTC 658
QY 337 CAGCGCCGCTTCGACGACCGCATGTCCGACACTTACACTTCTACTCGGCGGACGAGCG 396
Db 659 AGCAATCGTACACAGGAACGCAAGGAGGAAAACACGAGAAGGACTGGACCAAGAAAGC 718
QY 397 GCGTGTGCGCGCGGAC-----GAGCGCGCGCGCGC 429
Db 719 CATGATGTGAGTACGACTCTCTGTTTGAAGAGTCTCTCTGTTTGAAGAAGAGCTGGAG 778
QY 430 GGGCCGAGGCGGCTCCCTCCAGGCGCTGTGAGGCGCATGCGGCGGACCTTCGAGGAG 489
Db 779 AAGTTTGACACACTCGCATTTGGTCACTCGGAAGAAATCTGGAATTAGATGAGAAAT 838
QY 490 CCCAGCTGCTGCTGGCGCGCGAGATCTCGCTAGCGTGTGCGTGTGCTGCTGATCGTG 549
Db 839 CCAGCGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 898
QY 550 TCCATGTGTGTGCTGCGCGCAGCAGCTTGCAGGCTGGCGCAACGAGCGCGGACAAAC 609
Db 899 TCCATGTGTGTGCTGCGCGCAGCAGCTTGCAGGATGTCAGATTCAGAAATGAGGATG 958
QY 610 CGCAGCTGATGACCGGAGCAGGATAAATGAAGCTATCTGCAATAGTGTGCTTCACTGCC 669
Db 959 GATGATCCGCTGCTGGAAGGAGTGGAGATCG-----CGTGCATTCCTGCTTCCCGGG 1012
QY 670 GAGTGCATCGTGGGTTCAATGTTCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTG 729
Db 1013 GAGCTGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
QY 730 AACATCATTTGATTTACTGGCAATCACGCGCTATTACATCTCTGTGTTGATGACAGTGT 789
Db 1073 AACATCATTTGATTTACTGCTTCTATTTATTTCTTCTATGCGACGTTGGCTGTAGACCA 1132
QY 790 ACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGAGGTACTTAGAATGATG 849
Db 1133 GAGGAAGAGAGTGGAGATATTGAAACATGCGCAAGGTGCTCCAGATCTTACGCTTATG 1192
QY 850 AGGATTTTGGGTTGATTAAGCTTGGCGCTCACTTCAATGCTTTCAGACACTCGGTTTG 909
Db 1193 AGGATTTTGGGTTGATTAAGCTTGGCGCTCACTTCAATGCTTTCAGACACTCGGTTTG 1252
QY 910 ACTCTCAAGCTTGTCTACCGAGAGATGTTATGTTACTTGTCTTCAATTTGTGTTGCCAT 969
Db 1253 ACCTGAGACACAGCTACCACTGAAGTTGGGCTTCTGCTTCTTCTTCTTCTGTTGGGAT 1312
QY 970 GCAATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGGCTGGACCTGGGAAACATCAAC 1029
Db 1313 TCCATTTTCTG-----TGCTTATCTCTCGTGGAGAAAGATGACCAACA 1360
QY 1030 AAGGACTTTTACAGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089
Db 1361 TCCAGCCTCCAGCACTCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420

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QY 1090 GGCTATGGAGATGATGATCTCTATCAGATCGCTGGAGAAATCTTTGAGGAGTTTGTGTT 1149  
 DB 1421 GGTATGGAGACACCCACCGGTCTCTTGGCGGAAAGCTCATCGCCAGCATGTCATC 1480  
 QY 1150 GTCAGTGAATTTCTTATTTGGCATTTACCTATACATCTTTTATCTTACATAGCTTTGGAG 1209  
 DB 1481 ATCTGTGGCATCTTGGTGGGCGCTTCCATCACCATCATCTTCAACAAGTTTCCAAAG 1540  
 QY 1210 TGTATCATGAGCTCAAG 1227  
 DB 1541 TACTACAGAAGCAAAAG 1558

RESULT 11  
 US-09-336-643A-5  
 ; Sequence 5, Application US/09336643A  
 ; Patent No. 6399761  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miller, Andrew P.  
 ; APPLICANT: Curran, Mark Edward  
 ; APPLICANT: Hu, Ping  
 ; APPLICANT: Rutter, Marc  
 ; APPLICANT: Wang, Jian-Wang  
 ; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
 ; FILE REFERENCE: SEQ-15P  
 ; CURRENT APPLICATION NUMBER: US/09/336,643A  
 ; CURRENT FILING DATE: 1999-06-18  
 ; PRIOR APPLICATION NUMBER: 60/076,687  
 ; PRIOR FILING DATE: 1998-08-07  
 ; PRIOR APPLICATION NUMBER: 60/116,448  
 ; PRIOR FILING DATE: 1999-01-19  
 ; PRIOR APPLICATION NUMBER: PCT/US99/03826  
 ; PRIOR FILING DATE: 1999-02-22  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 2293  
 ; TYPE: DNA  
 ; ORGANISM: H. sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (330)...(1800)  
 ; OTHER INFORMATION: K-Hnov6  
 US-09-336-643A-5

Query Match 11.4%; Score 146; DB 4; Length 2293;  
 Best Local Similarity 48.0%; Pred. No. 2.3e-24;  
 Matches 585; Conservative 0; Mismatches 585; Indels 48; Gaps 4;  
 QY 37 CTGACCTGGCGCGCGCGTATTGCTGCTCCGGGAGCTGCTGAAGACTTCCCGCTG 96  
 DB 384 CTGAATGTGGGGCTTTTAAGCAGTCTGTTGAACAAGCAACCTCTCTGGGTTCTCTAC 443  
 QY 97 CGCGCGTGTAGCGGCTGCAACGCTGCGCTGCGAGCGGACGCTGCTCGAGGTGTGCGAC 156  
 DB 444 ACCAGACTGGGAAGCTGCTTACTTGCCATTTGAAGAGGCCATCTCGAGCTGTGTGAT 503  
 QY 157 GACTACACCGGAGCGCAAGTACTTCTTACCGCGCACTCGGAGGCTTCGGCTTC 216  
 DB 504 GATTACAGTGTGGCGGATAAGGAATACTACTTGATCGGAATCCCTCTTTGTTACATAT 563  
 QY 217 ATCTGCTCTACGTGCGCGCGCAACGCTGCTGCTGCGCGCGGAGTGTGCGAGCTC 276  
 DB 564 GTTTTGAAT--TTTATTACAGGGGAAGCTCATGTCTATGAGGAGCTGTGCGTATTC 620  
 QY 277 TCTTCTTACACAGATGATCTACTGGGCGCTGGAGGCGCGCACTCTGAGTACTCTGCG 336  
 DB 621 TCATTCTGCCAGGATCTGAGTACTGGGGCATCAACGAGCTCTTCAATGATCTTCTGCTGC 680  
 QY 337 CAGCGCGCTCTCAGACCGCATGTCTCGACACCTTACCTTCTACTCGGCGGACGAGCGG 396  
 DB 681 AGCAATCGCTACCAAGAACGACGAGGAGGAAACCAACGAGAGGACTGGGACCAAGAACG 740

QY 397 GGCTGCTGGCGCGCGAC-----GAGGCGCGCGCGCGC 429  
 DB 741 CATGATGTGATACCGACTCTCTGTTTGAAGAGTCGTCCTGTTTGAAGAAAGAGCTGGAG 800  
 QY 430 GGGCCGAGGGGGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGGCGACCTTCGAGGAG 489  
 DB 801 AAGTTTGACACACTGCGATTGCTGAGCTCCGGAAGAAATCTGGATTGAATGGAGAAT 860  
 QY 490 CCCACGCTGCTGCTGGCGCGCGAGATCCTGCTAGCTGCTGGTGGTGGTGGTGGTGGTGGT 549  
 DB 861 CCAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920  
 QY 550 TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609  
 DB 921 TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980  
 QY 610 CGCAGCTGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGTGTGCTGCTGCTGCTG 669  
 DB 981 GATGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1034  
 QY 670 GAGTGCATCTGAGGTTTCTTCTTCCAAACAAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTG 729  
 DB 1035 GAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1094  
 QY 730 AACATCATGTTTACTGGCAATCAGCCGCTATACATCTCTGCTGCTGCTGCTGCTGCTGCTG 789  
 DB 1095 AACATCATGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1154  
 QY 790 ACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGAAGGCTGCTGCTGCTGCTGCTG 849  
 DB 1155 GAGGAAGAGAGTGAAGTATGAGAACATGGGCAAGTGTCCAGATCTTACGCTTATG 1214  
 QY 850 AGGATTTTGGGTGATTAAGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909  
 DB 1215 AGGATTTTCCGAATTTAAAGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1274  
 QY 910 ACTCTCAAAAGTCTACCGAGAGATGTTATGTTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTG 969  
 DB 1275 AACTGAGACAGACTACCATGAAGTTGGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTG 1334  
 QY 970 GCAATCTTTAGTGCATTTCTCAGCTTCTTGAACATGGGCTGAGCTGCTGCTGCTGCTGCTGCTG 1029  
 DB 1335 TCCATTTTCTCTG-----TGCTTATCTACTCCGTTGGAGAAAGATGACCAACA 1382  
 QY 1030 AAGGACTTTACAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089  
 DB 1383 TCCAGCTTACAGCACTTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1442  
 QY 1090 GGCTATGAGATATGATATCTTATCAGAGTGCCTGGAAGAAATCTTGGAGGAGTTTGTGTT 1149  
 DB 1443 GGCTATGAGACACCCACCGCTTCCCTTGGCGGAAAGCTCATCGCCAGCAGCATGCTATC 1502  
 QY 1150 GTCAGTGAATTTGTTTATTTGGCACTTACCTATCTTCTTCTTCTTCTTCTTCTTCTTCTG 1209  
 DB 1503 ATCTGTGCACTTGTGGTGGGCGCTTCCCATCACCATCATCTTCTTCTTCTTCTTCTTCTTCTG 1562  
 QY 1210 TGTATCATGAGCTCAAG 1227  
 DB 1563 TACTACAGAAGCAAAAG 1580

RESULT 12  
 US-09-016-434-169  
 ; Sequence 169, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 955-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 169:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BRAINOT12  
CLONE: 1413667  
US-09-016-434-169

Query Match 9.5%; Score 122; DB 4; Length 267;  
Best Local Similarity 68.8%; Pred. No. 3.9e-19;  
Matches 183; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

QY 48 CGGCGCCGGTATTGCTGCTCCGGGAGCTGCTGAAGGACTTCCGCTGCGCGGCTGAG 107  
Db 1 CGGCATCAAGTACTGCTGCTCCCTGGACACGCTGACGAGTTCGCGCTGACGCGCTGG 60  
QY 108 CCGGCTGACGCTGCGCTCCGAGCGGACGTGCTCGAGGTGTCGACGACTACGACCG 167  
Db 61 CCAGCTCAAGGCTGCACCAACTTCGACGACATCCTCAACGCTGCGATGACTACGAGT 120  
QY 168 CGAGCGCAACGAGTACTTCTTCGACGGCACTCGGAGGCTTCGGCTTCATCTCTCTA 227  
Db 121 CACCTGCAACGAGTCTTCTTCGACCGCAACCGGGGCTTCGGGACTATCTGACCTT 180  
QY 228 CGTGCGCGCCACGCAAGCTGCTTCGCGCGCGGATGTCGAGCTCTCCTCTCAAA 287  
Db 181 CTGCGCG--CGGCAAGCTGCGCTGCTGCGCGAGATGTCGCGCTGCTCTCCAGGA 237  
QY 288 CGAGATGATCTACTGGGCGCTGAGG 313  
Db 238 CGAGCTGCTGTACTGGGCGATCGCG 263

RESULT 13  
US-09-181-339-8  
Sequence 8, Application US/09181339  
Patent No. 6610827  
GENERAL INFORMATION:  
APPLICANT: Forsayeth, John R.  
APPLICANT: Zhao, Byron  
APPLICANT: Chavez, Raymond C.  
TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE  
TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR  
FILE REFERENCE: 5865-0033.30

CURRENT APPLICATION NUMBER: US/09/181,339  
CURRENT FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: US 60/063,450  
PRIOR FILING DATE: 1997-10-29  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 1273  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)...(1273)  
US-09-181-339-8

Query Match 9.0%; Score 115.4; DB 4; Length 1273;  
Best Local Similarity 50.3%; Pred. No. 2e-17;  
Matches 377; Conservative 0; Mismatches 351; Indels 21; Gaps 3;

QY 482 TCGAGAGAGCCACGTCGCTGCGCGCGCAGATCCTGGCTAGCGTGCCTGGTGTTCG 541  
Db 318 TGGAGAAATCCAGCGTACTGCTGTCGCTAAGCTTATCGCTATCTCTCTGAGCGTGG 377  
QY 542 TGATCGTGTTCATGGTGTGCTGTGCGCCAGCAGTTCGCCGACTGCGGCAACGACCG 601  
Db 378 TGCTGGCTCCATGCTGCGCATGTCGCTTCACAGCATGTCGAGTTCAGAAATGAGATG 437  
QY 602 CCGACAAACCGCAGCCTGGATGACCGGAGCAGGATAATGAAGCTATCTGCATAGTGTGGT 661  
Db 438 GAGAGTG-----GATGATCCGGTGTGGAAGAGTGGAGATCGCGTGCATTCGCTGGT 491  
QY 662 TCAGTCCGAGTGCATCGTAGGTTTATGTTCTCCAAAAACAAGTGTGAGTGTGTCAGA 721  
Db 492 TCACCGGGGAGCTTGGCGTCCGCTGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 551  
QY 722 GACCCCTGAACATCATGATTATCTGSCAATCAGCGCTATTACATCTCTGTGTGATGA 781  
Db 552 ACCCTCTGAACATCATGATTATCTGTTCTATATCTCTCTCTCTCTCTCTCTCTCTCT 611  
QY 782 CAGTGTGTTACAGCGCAGAACTCTCACTCCAGAGGCTGGAGTCACTTG---AGGTAC 838  
Db 612 GACACCAAGGAGGAAGAGAGTGAAGGATATGAGAAACATGGGCAAGGTGGTCCAGATCC 671  
QY 839 TTAGATGATGAGGATTTTGGGTGATTAAAGCTTGGCGCTCACTTCATTTGGTCTTCAGA 898  
Db 672 TAGCGCTTATGAGGATTTTCCGAAATCTAAAGCTTGGCGGCTCGGTAGGACTTCGGT 731  
QY 899 CACTCGGCTTGAATCTCAAAAGCTTGTACCGAGAGATGTTATGTTACTTCTCTCTCTCT 958  
Db 732 CTCTAGTGCCACACTGAGACAGCTACCATGAAGTTGGTTCCTCTCTCTCTCTCTCT 791  
QY 959 GTGTGCTGAGCAATCTTTAGTGCATTTCTCAGCTTCTTGAACATGGGCTGGACCTGG 1018  
Db 792 CTGTGGCAATTTCTCTCTG-----TGCTTATCTACTCCGTGGAGAAAG 839  
QY 1019 AAACATCAACAAAGGACTTTACAGCAGCATCTCTGCTGCTGCTGGTGGTGAATATCTCTA 1078  
Db 840 ATGACCAACATCCAGCTCACCAGCATCCCATCTCTGCTGGTGGTGGCCACCATAGCA 899  
QY 1079 TGACTACAGTGGCTATGGAGATATGATCTATCAAGTGCCTGGAGAAATTTCTGGAG 1138  
Db 900 TGACAACTGTGGGCTATGGAGACACCCACCGCTGCTTGGCGGGAAGCTCATCGCCA 959  
QY 1139 GAGTTTGTGTGTCAGTGAATTTCTTATTGGCATTACCTATCCTTTTATCTACCATTA 1198  
Db 960 GCATGATCATCTGTGGCATCTTGTGTGGCTTCCATCCATCCATCATCTTCAACA 1019  
QY 1199 GCTTTGTGCAAGTGTATCATGAGCTCAAG 1227  
Db 1020 AGTTTCCAAAGTACTACCAAGCAAAAG 1048

RESULT 14

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US-10-162-012-7
; Sequence 7, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1338)
US-10-162-012-7

Query Match      8.9%; Score 113.4; DB 4; Length 1341;
Best Local Similarity 47.0%; Pred. No. 5.9e-17;
Matches 508; Conservative 0; Mismatches 546; Indels 27; Gaps 4;

Qy 152 GCACGACTACGACCGGAGCGGAGTACTTCTTCGACCGGCGGAGGCGGAGGCGGCTTCG 211
Db 107 GCCGCTTCTACGACGCGGCGGCGGAGTATTTCTTCGACCGGCGGAGGCGGAGGCGGCTTCG 166

Qy 212 GCTTCATCTGCTCTACGTCGGCGGCGGAGCGGAGTCTTCGCGGCGGCGGAGTCTCG 271
Db 167 ACGCCGTGCTCTACTACGATCCAGTCCGGTGGCGGCGGCGGAGTCTTCGCGGCGGCGGAGTCTCG 226

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QY 272 AGCTCTCTCTTCAACGAGATGATCTACTGGGCGCTGGAGGGCGGCGCACCT-----CG 325
Db 227 TCAGCGTCTTCTCGAAGAGGTGCGCTTCTACGGGCTGGGCGGCGGCGGCGCTTGGCAGCC 286
QY 326 AGTACTGTGTCGACGCGGCTCGACGACGCGATGTCGACACCTACACCTTCTACTCGG 385
Db 287 TCGCGAGGAGGAGGTGCGCGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 346
QY 386 CCGACGAGCGGCGGCTGCTGGGCGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 445
Db 347 CCGCGGAGGCTGCGCTGCTTTTCGAGTTTCCCGAGAGCTCTCAGGCGGCGGCGGCGGCGG 406
QY 446 CCTCCAGGCGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 505
Db 407 CCGTAGTCTCGGTGCTGCTATCTCTGCTCTCCATCTGCTCTCTCTCTCTCTCTCTCTCT 466
QY 506 CCGCGGAGATCTGGCTAGGCTGTCGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565
Db 467 CTGACTTCCGCGACGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 526
QY 566 GCGCGGAGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 619
Db 527 TCCCGGCTCGGCTGAATGGGCTCCAGCCAAATGCTTGAATTCACCCCGGCTGCCCTTCA 586
QY 620 ATGACCGGAGCAGGATTAATGAAGCTATCTGCATAGGTTGGTTCACTGCCGAGTGCATCG 679
Db 587 ATGACCGGTTCTTCGTGCTGGAGACGCTGTGTATTTTGTGTTCTCTCTCTCTCTCTCT 646
QY 680 TGAGGTTCAATGCTCCAAAACAAAGTGTGAGTTGTCAAGAGACCCCTGAAATCATCTG 739
Db 647 TAGCGCTCTGCTGTCTCAAGCAAGGCTATCTTCTCAAGAACGATGAAGCTCATCG 706
QY 740 ATTTACTGGCAATCACGCGGCTATTACATCTCTGTGTGA--TGACAGTGTTTTACAGGCG 796
Db 707 ATTTGTGGCTATCTTCCCTACTTTTGTGCACTGGGCACTGGGCGGCGGCGGCGGCGGAG 766
QY 797 AGAATCTCTAACTCCAGAGGCGGCTGAGTCACTTGGGCTGAGTGTAGTGTAGTGTAGTGT 856
Db 767 GGGTGGGCGGAGCAGGCGGCTGCTACTGGCCATCTCTGAGAGTCACTCCGATTTGGTGTCT 826
QY 857 TTTGGGTGATTAGCTTGGCGGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 916
Db 827 TCCGCACTTCAAGCTGTCCGCGCTCAAGGCGCTGCAAACTCTTGGGCGGCGGCGGCGGCT 886
QY 917 AACGTTGCTTACCGAGAGATGTTATGTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 976
Db 887 GGGCTCCATGCGTGGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 946
QY 977 TTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGAGCTTGAACACATCCACAGGAGCT 1036
Db 947 TTTCCAGGCGGCTGCTATTTGCCGAGTTGACCGGTTG-----ACTCCCAT 994
QY 1037 TTACGACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1096
Db 995 TCATAGCATCCCTGAGTCTCTTGTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
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QY 1217 A 1217
Db 1175 A 1175

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; Patent No. 5610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5855-0033.30
; CURRENT APPLICATION NUMBER: US/09/181.339
; PRIORITY FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1647)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2799)
; OTHER INFORMATION: n = A,T,C or G
US-09-181-339-2

Query Match      8.4%; Score 107.8; DB 4; Length 2799;
Best Local Similarity 48.1%; Pred. No. 1.4e-15;
Matches 620; Conservative 0; Mismatches 567; Indels 102; Gaps 7;

QY 9 CGGGCGACGCGGGCGGCTCGTGTGTGCTGAACGTGGGCGGCGCGGTTATCGCTGTC 68
DB 192 CTGGCGGCTAGACGARGCGCTCGGCTGAACGTGGGCGGAGTGGCGGCGTCTGAG 251
QY 69 CCGGAGCTGTGAAGGACTCCCGCTGCGCGCTGAGCGGCTGACGCGCTGCGGCTC 128
DB 252 CCGCGCGCGGCTGTGGCGCTTCCCGGCGACGCGCTGTGGCGGCTTACAGCGCGGCGCTC 311
QY 129 CGAGCGGACGCTGTGCGAGCTGTGCGAGCTACGACCGCGCGGCGCAACGAGTACTTCT 188
DB 312 CGAGGAGCAGCGCGGCGGCTGTGCGAGCTACGACGCGGCGGCGAGTCTTACTT 371
QY 189 CGACGGGCACTCGGAGGCTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
DB 372 TGATCGGCATCC---GGGCTTCTTCTCGGCGTCTTACACTTCTACCGCGCGGCACT 428
QY 249 GCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTACTGGGCGCT 308
DB 429 GCAGCTCTAGAGAGCTGTGCTTCTGCTTCTGCGCTTCCGCGAGAGGCTGACTACTGGGCGCT 488
QY 309 G---GAGGCGCGCACCTCGAGTACTGTGCGAGCGCGCGGCTGCGAGCGGCGATGTCGA 365
DB 489 GGGCGAGAACGGCTGGCCACGCTGCTGCGCGCGCGGCTATCTGGAGCGGCGGTGTGGCGCG 548
QY 366 CACCTACACTTCTACTCGGCGGCA---GGGCTTCTTCTCGGCGTCTTCTTCTTCTTCTTCT 401
DB 549 GCGTCGCGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
QY 402 GCTGGGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 461
DB 609 GATCTCGAGCGTGCAGCGGAGCTGGCGGCTATGTGCGGCTGCTGTGGCGCGCTGCG 668
QY 462 GGAGCGGATGCGGCGGAGCTTGGAGAGCGGCGGCTGCTGCTGCGGCGCGGCGGCGGCGGCG 521
DB 669 CCGTCGCTCTGCGCTCACCATGAGAGATCCAGGCTACTCGCTGCCGAGGAGCTCTTCTGAG 728
QY 522 TAGCGGTGCGGTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
DB 729 CTGCGTATCCATCGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 788
QY 582 CGACT-----GGCGCAACCGAGCGCGCGGCAACCGGAGCT 617
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DB 789 GGAGTACCAAGCTCGGGAGGCGGCGGCTGCGAGTGGCGGCGGCTGCGAGCGC 848
QY 618 GGATGACCGGAGC-----AGGATAATTGAAGCTATCTGCATAGGTGGTT 662
DB 849 AGAGGAGGTGCGGAGGAGCCCGGTGCTGCGCGCTGGAGTACTTCTGATCGTGGTT 908
QY 663 CACTGCCGAGTGCATCGTGAAGGTTCATTGCTCTCCAAAAAAGAGTGAATTTGTCAAGAG 722
DB 909 CAGCTTCGAGGTGCTGCTGCGGCTGCTGCGGCTCCACGACGCGCAACTTCTTCTGCCA 968
QY 723 ACCCTTGAACATCATGATTTACTGCAATCAGCGGTATACATCTCTGTGTGATGAC 782
DB 969 CCGCTCAACCTCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1028
QY 783 AGTGTTTTACAGCGGAGAACTCTCACTCCAGAGGCTGGAGTCACT-----829
DB 1029 CGCAGCGCTTGTGACCGAGCGGAGCGGAGGAGCTCGGGGACCTGGGCAAGGT 1088
QY 830 --TGAGGTACTTAGAATGATGAGGATTTTGGGTGATTAGCTTGCCTGCCTCATTCT 887
DB 1089 AGTGAAGTGTTCGCGCTCATGCGCATCTTCGCGTGTCTAAGCTGGCGGCGCATCTTACT 1148
QY 888 TGGTCTTCAGACACTCGGTTTGAATCTCAAACTTGTCTACCGAGAGATGTTATGTTACT 947
DB 1149 GGGCTGCGTTCGCTGGCGGCGGCTCAAGCACAGCTACCGTGAAGTGGGCTTACT 1208
QY 948 TGTCTTCATTGTTGTGGCCATGCAATCTTTAGTGCATCTTCTCAGCTTCTTGAACATGG 1007
DB 1209 GCTGTACTTGGCGCTGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1265
QY 1008 GCTGGACTGGAACATCCAAAGGAGCTTTACAGCATCTCTGCTGCTGCTGCTGCTGCTGCT 1067
DB 1266 -----AGAAAACGAGGCTTTCACAACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1310
QY 1068 GATTATCTTATGACTACAGTTCGCTATGAGATATGATTCCTATCAAGTGCCTGGAAG 1127
DB 1311 CACAGTGAAGCATGACCAAGTGGGCTATGGGATGTGGTCCAGAGACTGTGGTGGCAA 1370
QY 1128 AATCTTGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1187
DB 1371 GCTGGCGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1430
QY 1188 TATCTACCATAGCTTTGTGCGAGTGTATC 1216
DB 1431 CATCTTCAACAGTTTTTCCCACTTCTACC 1459
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Search completed: October 6, 2004, 20:35:57  
Job time : 127 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 6, 2004, 16:28:11 ; Search time 3653 Seconds  
(without alignments)  
10447.267 Million cell updates/sec

Title: US-10-016-647-1  
Perfect score: 1278  
Sequence: 1 atgaccttcggggcagcgg.....ccactgaattcctgaattaa 1278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estrov:\*
- 6: em\_estrpl:\*
- 7: em\_estro:\*
- 8: em\_hrc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hrc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_nam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_fod:\*
- 26: em\_gss\_pbg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	444.6	34.8	523	9 AI043703	AI043703 UI-R-CO-j
2	437.4	34.2	500	28 AQ402619	AQ402619 HS_5086A
3	433.6	33.9	509	29 CG639652	CG639652 OST371309
4	398	31.1	484	29 CG662016	CG662016 OST444129

5	386	30.2	971	29	CNS0206W	AL175217 Tetraodon
6	361.4	28.3	772	13	BU274588	BU274588 603533001
7	353	27.6	487	29	CG582101	CG582101 OST222985
8	264.4	20.7	2562	29	AY417320	AY417320 Mus muscu
9	260.6	20.4	2565	29	AY417318	AY417318 Homo sapi
10	247.2	19.3	1028	29	CNS04AK5	AL303998 Tetraodon
11	239	18.7	298	9	AI137172	AI137172 UI-R-C2p-
12	213.2	16.7	301	29	CE495701	CE495701 tigr-gss-
13	200.4	15.7	652	12	BJ495239	BJ495239 BJ495239
14	194.6	15.2	505	29	FR0030615	AL013498 F.rubripe
15	193.8	15.2	887	10	BF966122	BF966122 602286371
16	191.2	15.0	242	29	CG580684	CG580684 OST220291
17	190.4	14.9	555	29	FR0020576	AL013459 F.rubripe
18	185.6	14.5	431	29	FR0020585	AL013458 F.rubripe
19	183.4	14.4	1476	29	AY415319	AY415319 Mus muscu
20	182.4	14.3	2936	11	AK046054	AK046054 Mus muscu
21	180.2	14.1	879	10	BE389327	BE389327 601286211
22	178.2	13.9	806	12	BF872101	BF872101 603396406
23	176.2	13.8	1503	29	AY398782	AY398782 Pan trogl
24	173.8	13.6	2360	11	AK087481	AK087481 Mus muscu
25	173.8	13.6	4111	11	AK048819	AK048819 Mus muscu
26	173.4	13.6	314	10	BF552004	BF552004 UI-R-C2p-
27	167.8	13.1	1503	29	AV398781	AV398781 Homo sapi
28	165.8	13.0	446	29	CNS04K0H	AL294218 Tetraodon
29	161.4	12.6	2530	29	AY417319	AY417319 Pan trogl
30	161.2	12.6	398	29	CG661991	CG661991 OST444030
31	160.8	12.6	906	13	BQ941236	BQ941236 AGENCOURT
32	155.8	12.2	529	10	BF058746	BF058746 7k34c08.X
33	155.6	12.2	1087	29	CNS02H90	AL197325 Tetraodon
34	154.8	12.1	262	29	CG661999	CG661999 OST444070
35	149.8	11.7	629	12	BM537328	BM537328 ha88c06.g
36	149.4	11.7	1297	12	BM805900	BM805900 AGENCOURT
37	148	11.6	954	12	BG750400	BG750400 602709235
38	146	11.4	1476	29	AY415317	AY415317 Homo sapi
39	143.2	11.2	682	13	BQ257115	BQ257115 NISC.ko10
40	141.6	11.1	166	29	CG513356	CG513356 OST66687
41	139.6	10.9	522	9	AV947539	AV947539 AV947539
42	136.4	10.7	655	10	AW826048	AW826048 us20f05.X
43	135.4	10.6	938	13	BQ946749	BQ946749 AGENCOURT
44	134.4	10.5	871	29	CNS03M1Y	AL250207 Tetraodon
45	134	10.5	990	29	CNS02EGS	AL193717 Tetraodon

ALIGNMENTS

RESULT 1  
AI043703  
LOCUS AI043703 523 bp mRNA linear EST 05-JUL-1999  
DEFINITION UI-R-CO-jl-g-04-0-UI-sl UI-R-CO Rattus norvegicus cdna clone  
UI-R-CO-jl-g-04-0-UI-3', mRNA sequence.  
ACCESSION AI043703  
VERSION AI043703.1 GI:3290438  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 523)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996).  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8350  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu



QY	857	TTTGGGTGATTAAGCTTTGCCCGTCACCTTCATTGGTCTTTCAGACACTCGGTTTGACTCTCA	916
DB	440	TTTGGGTGATTAAGCTTGCCAGTCACCTTCATTGGTCTTTCAGACACTCGGTTTGACTCTCA	381
QY	917	AAGCTTGCTACCGAGAGATGGTTATGTTACTTGTCTTCATTGGTTGCCATGGCAATCT	976
DB	380	AAGCTTGCTACCGAGAGATGGTTATGTTACTTGTCTTCATTGGTTGCCATGGCAATCT	321
QY	977	TTAGTGACACTTTCTCAGCTTCTTTGAACATGGGTGGACCTGGAAACATCAACAAGGACT	1036
DB	320	TTAGTGACACTTTCTCAGCTTCTTTGAACATGGGTGGACCTGGAAACATCAACAAGGACT	261
QY	1037	TTACCAGCATTCCTGCTGCTGCTGGTGGGTGATTATCTCTATGACTACAGTTGGCTATG	1096
DB	260	TTACCAGCATTCCTGCTGCTGCTGGTGGGTGATTATCTCTATGACTACAGTTGGCTATG	201
QY	1097	GAGATATGTTATCCTATCACAGTGCCTCGAAGAAATCTTGGAGAGAGTTGTGTTGTCTCAGT	1156
DB	200	GAGATATGTTATCCTATCACAGTGCCTCGAAGAAATCTTGGAGAGAGTTGTGTTGTCTCAGT	141
QY	1157	GAATTTGTTCTATGGCAATTACCTATCACTTTTATCTACCATAGCTTTGTGTCAGTGTATC	1216
DB	140	GAATTTGTTCTATGGCAATTACCTATCGCTTTTATACAAAAGACTTTGTGCAGTGTATC	81
QY	1217	ATGAGCTCAAGTTTATAGTCTGTCAGGTATAGTAGGAGCCTCTCCACGAATTC	1269
DB	80	ATGAGCTCAAGTTTATAGTCTGTCAGGTATAGTAGGAGCCTCTCCAGTACTAC	28
RESULT 3	CG639652	509 bp DNA linear GSS 02-OCT-2003	
LOCUS	OST371309	Mus musculus 129Sv/Ev Mus musculus genomic clone	
DEFINITION	OST371309	genomic survey sequence.	
ACCESSION	CG639652		
VERSION	CG639652.1	GI:37463501	
KEYWORDS	GSS.		
SOURCE	Mus musculus		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 509)		
	Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,		
	Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,		
	Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,		
	Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,		
	Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,		
	Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,		
	Zhu, Q., Person, C. and Sands, A.T.		
TITLE	Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap		
JOURNAL	screen to identify potential targets for therapeutic intervention		
COMMENT	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)		
	Contact: Zambrowicz BP		
	OmniBank		
	Lexicon Genetics Incorporated		
	4000 Research Forest Drive, The Woodlands, TX 77381, USA		
	Email: material@lexgen.com		
	Gene trap sequence tag generated by 3' RACE from mouse ES cells as		
	described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)		
	Class: Gene Trap.		
FEATURES	Location/Qualifiers		
source	1..509		
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Query Match	33.39%	Score 433.6;	DB 29; Length 509;



QY 848 TCAGGATTTTGGGTGATTAAAGCTTGCCCTCACTTCATTGGTCTTCAGACATCGGTT 907  
 DB 638 TGAGGATCTTCTGGGTGATCAAGCTAGCGGTCACTTCTCGGCTCGACAGCTCGGCC 697  
 QY 908 TGACTCTCAACAGTTGCTACCGAGAGATGGTTATGTACTTGTCTTCACTTGTGTTGCCA 967  
 DB 698 TGACGCTTCGACGCTGCTACCGGAAATGATGCTCTCTGCTTCTCATCTGCGTTGCCA 757  
 QY 968 TGGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAACATGGGCTCGACTCGAATCCCA 1027  
 DB 758 TGGCGATCTTCAAGTGCACTGACAGAGCTGCTGGAGCAGCGCTCGACTTGAAGCGGAA 817  
 QY 1028 ACAAGGACTTTTACCAGCAATCTCTGCTGCTGCTGCTGGGTGATTTCTTATGACTACAG 1087  
 DB 818 ACCAGGACTACCGCAGCTCCCGCAGCGCTGCTGGGTGATCATCTCTCCATGACGCG 877  
 QY 1088 TTGGGTATGGAGATATGATCTATACAGTGCCTGGAGAAATCTTGGAGAGCTTTGTG 1147  
 DB 878 TGGGTACGGGACATGTACCGGTGACGGTGGCAGCGCGGCTGCTGGGCGGCTGTGCG 937  
 QY 1148 TTGTCAGTGGAAATCTTCTATTGGCATTAACCTAT 1181  
 DB 938 TTGTGAGCGGGATCGTKTCTGTGCGCTGCCCAT 971

RESULT 6  
 LOCUS BU274588 772 bp mRNA linear EST 26-NOV-2002  
 DEFINITION 603533001F1 CSEQHN53 Gallus gallus cDNA clone CHEST490a2 5', mRNA  
 sequence.  
 ACCESSION BU274588  
 VERSION BU274588.1 GI:25545538  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 772)  
 AUTHORS Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,  
 Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers

FEATURES  
 source  
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 /organism="Gallus gallus"  
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 /db\_xref="taxon:9031"  
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 /note="Organ: brain; Vector: pBluescript II KS(+); Site\_1:  
 ECoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunt-ended, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 28.3%; Score 361.4; DB 13; Length 772;  
 Best Local Similarity 81.3%; Pred. No. 3.5e-50;  
 Matches 482; Conservative 0; Mismatches 101; Indels 10; Gaps 5;  
 QY 632 GGATAATTGAAGCTATCTGCATAGTGTGTTCACTCCGAGTGCATCGTAGGTTCAATTG 691  
 DB 130 GGATAATTGAAGCTATCTGCATAGTGTGTTCACTCCAGAGTGCATGTGAGGTTCAATCG 189  
 QY 692 TCTCCAAAACACAGTGTGAGTTGTCAAGAGACCCCTGAACATCATTTGATTACTGGCAA 751  
 DB 190 TTTCAAAGAACACAGTGTGAGTTGTGAGAGACCTCTCAACATTAATGATTACTGGCAA 249  
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 DB 250 TTACTCTTACTACATCTCTGTTCTAATGACAGTGTTTACAGGGGAAAATTCGCAACTCC 309  
 QY 812 AGAGGGCTGGAGTCACTCTGAGGTACTTAGATGATGAGGATTTTGGGTGATTAAAGC 871  
 DB 310 AGAGGGCTGGAGTCACTCTTGAAGGTCTTAAGAAATGATGAGGA--TTTGGGTGATTAAAC 367  
 QY 872 TTCCCGCTCACTTCATTGTTCTTACAGACACTCGGTTTGACTCTCAAAACGTTGTCACCGAG 931  
 DB 368 TGCTGCTCATTTCAATGGCTTCAACACATTTGTTGCTGACTCTGAAGCGTGTGACAGAG 427  
 QY 932 AGATGGTTATGTTACTTGTCTTCAATTTGTTGTTGCCATGGCAATCTTTAGTGCACTTCTC 991  
 DB 428 AGATGGTGTGTCCTTGTCTTTATCTGTTGCTATGCGCAATTTTCAGTGCATTTCC 487  
 QY 992 AGTCTCTGAACATGGCTGGACCTGGAACATCCAAAGAGACTTTACCAGCATTCCTG 1051  
 DB 488 AGTCTTGAAATGGCTGGACTTTGGGACAAAGAAATAGGATTAAGCAGATCCCTG 547  
 QY 1052 CTCGCTGCTGGTGGGTGATTATCTCT-ATGACTACAGTTGGCTATGGAGATATGATTCCT 1110  
 DB 548 CTCGCTGGTGGTGGGTGATCATCTCTCATGACCACAGTGTGTTACGCTGCATGTGTCCC 607  
 QY 1111 ATCACAGTGCCTGGA--GAATTCCTGGAG--AGTTGTTGTTGCTGAGTGAATTTCT 1166  
 DB 608 ATCACAGTACCGGAAAGGATTTCTTGGAGGAAATCTGCGTGGTGTAGTGGCATCGTTT 667  
 QY 1167 ATTGGCATTAACCTA---TCACCTTTTATCTACCATAGCTTTGTGCACTGTTTATC 1216  
 DB 668 ACTAGCCCTTGCCAAATCACCTTTCATTATCATAGCTTTGTGCACTGTTTACC 720

RESULT 7  
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 DEFINITION OST222985 Mus musculus 129Sv/Ev Mus musculus genomic clone  
 OST222985, genomic survey sequence.

ACCESSION CG582101  
 VERSION CG582101.1 GI:37379484  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 487)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Zambrowicz, B. P., Abuin, A., Ramirez-Solis, R., Richter, L. J.,  
 Piggott, J., BeltrandelRio, H., Buxton, E. C., Edwards, J., Finch, R. A.,  
 Fiddle, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
 Key, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
 Payne, R., Potter, D. G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
 Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,





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605 TGTCACACACACTGCTGAGCTACAGAGCTGACGAATCGGCCAGACGACGACA 664
623 ACCGAGCAGGATA---ATTGAAGTATCTGATAGTGGTTCATCTGCGGAGTGCATCG 679
665 ACCGAGCTGGCACAGTGGAGGTGTGTGATCGGTGGTTCACCATGGAGTACTTGC 724
680 TGAGGTTCATCTCTCCAAACAGTGTGATTTGTCAAGAGCCCTGACATCATNTG 739
725 TGAGGTTCCTGCTCCGCGCCCAAGAAATGGAAGTCTTTAAGGCGCCCTCAACGCCAT 784
740 ATTACTGGCAATCAGCCGCTATTACATCTCTGTGTGTATGACAGTGTTTACAGCGAGA 799
785 ACTTACTGACCATCTGCTGCTACTACTAGTCAACATCTTCTCAGAAATCCACAGAGCG 844
800 ACTCTCACTCAGAGGGGTGAGTACACCTTGAGGGTACTTAGAATGATGAGGATTTTT 859
845 TGCTGAGTTCAGAAATGTGCGCGGTGTGTCAGATCTTCCGATCATGCGCATCCTGC 904
860 GGTGATTAAGCTTGCCCGTCACTTCAATGCTTTCAGACACTCGGTTTGAATCTCAAA 919
905 GCATCTGAGTGTGCGCCGCACTCCACCGTCTGAGTCTTGGGCTTCAAGTGGCGCA 964
920 GTTGTACCGAGAGATGTTATGTTACTTGTCTTCAATTTGTTGCTGCAATGCAATTT 979
965 GGAGCTACAAACGAGCTGGGCTTGTCTCATCTCTCTGCGCATGGGATCATGATCTT 1024
980 GTGCACTTCTCAGCTTCTTGACATGCGCTGAGCTGGAACATCCACAGGACTTTA 1039
1025 CCAGCTGTGCTTCTTTCGCGAGAGGATGAGGA-----TGACCAAGTTCA 1072
1040 CCAGCATCTCTGCTGCTGCTGGTGGTGAATATCTATGACTACAGTTGGCTATGAG 1099
1073 AAAGCATCCCGCTCTTCTGCTGGCTTACCATCAGCATGACGACCGTGTGTTACGG 1132
1100 ATATGATCTCTATCAGCTGCTGAGAGATTTCTTGGAGAGTGTGTTGCTAGTGAA 1159
1133 ACATCTACCTAAGACTCTCTGCGGGAATCTGCGGGGCTCTGTTGCAATGCGGCT 1192
1160 TTGTTCTATTTGCAATACCTATCACTTTTATCTACATAGCTTTGTCAGTGTATCAT 1219
1193 TCTGTTGATGCTCCCTCCCATCCAAATATGTCATTAATCTTCCGAGTTCTACAAG 1252
1220 AGCTCAAG 1227
1253 AGCAGAAG 1260

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RESULT 9
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LOCUS
DEFINITION
Homo sapiens KCNB1 gene, 2565 bp DNA linear GSS 17-DEC-2003
genomic survey sequence.
ACCESSION
AY417318
VERSION
AY417318.1 GI:39773278
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2565)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
JOURNAL
PUBMED
2 (bases 1 to 2565)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

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TITLE
JOURNAL
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>2565
/genes="KCNB1"
/locus_tag="HCM6184"
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Best Local Similarity 53.7%; Pred. No. 3e-33;
Matches 645; Conservative 0; Mismatches 529; Indels 27; Gaps 4;
QY 30 GGTGGTCTGAACGTGGCGCGCCCGGTTATTCGCTGCCGGGAGCTGCTGAGGACTT 89
DB 84 GGTCCGCTCAACAGTCCGGGGGTGGCGCAGAGGTACTCTGGCGTACCTGGACCGCCT 143
QY 90 CCCGCTCGCGCTGAGCGCGGTGCACGGCTGCCGTCGAGCGCGACCGTGTCTGAGGT 149
DB 144 GCCCGCACGGCTGGGCAAGCTCCGCGACTGCAACACGACGACTCGTCTCGAGGT 203
QY 150 GTGCGAGCATACGACCGGAGCGCAAGAGTACTTCTTCGACCGGACTCGGAGGCTT 209
DB 204 GTGCGATGACTACGACCTCGACGACACGAGTACTTCTTTCGCGCCACCGCGCGCTT 263
QY 210 CGGCTTCATCTGCTCTACGTCGCGCCACGCAAGCTCGCTTCGCGCGCGGATGTG 269
DB 264 CACTCCATC---CTCAACTTCTACGCACTGGGCACTGCATGATGAGGAGATGTG 320
QY 270 CGAGCTCTCTTTACAAAGAGATGATCTACTGGGCTTGGAGGGCGGCACTTCGAGTA 329
DB 321 CGCGCTCAGCTTCAGCCAGAGTCTGACTACTGGGCACTGCGAGATCTACCTGAGTC 380
QY 330 CTGCTGCCAGCGCGCTCGACGACCGCATGTCCGACCTACACCTTCTACTCGGCGA 389
DB 381 CTGCTGCCAGCGCGCTTACCACCA-----GAGAAAGAGCAGATGAACGAGGACT 431
QY 390 CGAGCCGGGCTGTGCTGGCGCGGACGAGGCGCGCCCGCGGGCGGAGCGGCTCCCTC 449
DB 432 CAAGCGTGAGCGGAGACCTTACGGGAGCGGAGGAGTTCGATAACACGCTGCTG 491
QY 450 CAGCGCTGCTGGAGCGCATGCGGGGACCTTCGAGGAGCCACGCTGCTGCTGGCGC 509
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DB 552 CAAGATCCTTGGCATAATTTCCATCATGTTTCATGTCCTCTCCACCATGCTGCTGCT 611
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QY 807 ACTCCAGAGGGCTGAGTCACTTGGGGTACTTAGAATGATGAGGATTTTGGGGTAT 866

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Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

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TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.  
 Fatima Bonaldo, Ph.D. Clone distribution: clones will be available  
 through Research Genetics This clone is also available through the  
 I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE  
 ID=1787504  
 Seq primer: M13 Forward  
 POLYA=No.

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 /dev\_stage="adult"  
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 /clone\_lib="UI-R-C2p"  
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 library, which is a subtracted library derived from the  
 UI-R-C0 library. The UI-R-C0 library consisted of a  
 mixture of individually tagged normalized libraries  
 constructed from rat placenta, adult lung, brain, liver,  
 kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day  
 embryo. The tag is a string of 3-5 nucleotides present  
 between the Not I site and the oligo-dT track which allows  
 identification of the library of origin of a clone within  
 the mixture. The subtracted library (UI-R-C2p) was  
 constructed as follows: PCR amplified cDNA inserts from  
 UI-R-C1 clones from which 3' ESTs had been derived was  
 used as a driver in a hybridization with the UI-R-C1  
 library in the form of single-stranded circles. The  
 remaining single-stranded circles (subtracted library) was  
 purified by hydroxyapatite column chromatography,  
 converted to double-stranded circles and electroporated  
 into DH10B bacteria (Life Technologies) to generate the  
 UI-R-C2p library. This procedure has been previously  
 described (Bonaldo, Lennon and Soares, Genome Research 6:  
 791-806, 1996)"

ORIGIN  
 Query Match 18.7%; Score 239; DB 9; Length 298;  
 Best Local Similarity 88.9%; Pred. No. 6.4e-30;  
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 QY 295 ATCTACTGGGGCTGGAGGGCGGCGACCTCGAGTACTGCTCCAGCGCGGCTCGACGAC 354  
 DB 298 ATCTACTGGGGCTGGAGGGCGGCGACCTCGAGTACTGCTCCAGCGCGGCTCGACGAC 239  
 QY 355 CGCATGTCCGACACCTTACTCGGCGCGAGCGCGGCGTGTGGGCGCGAC 414  
 DB 238 CGCATGTCCGACACCTTCCAGCGGCGAGAGGA-----GCTGGGCGCGAG 188  
 QY 415 GAGGCGCGCGCGGCGGCGGCGGCTCCCTCCAGCGCTGCTGAGCGGCTGCGG 474  
 DB 187 CAGCTCGTCCACCGGGCGGAGCGGCTCCCTCCGCGCTGCTGAGCGCATGCGG 128  
 QY 475 CGGACCTTCGAGGAGCCACGTCGCTGGCTGGCGGCGAGATCCTGGCTAGCGTGC 534

Db 127 CGGACCTTCGAGGAGCCACGTCGTCGTCGCGCGAGATCCTGGCCAGCGTGTCCGTG 68  
 QY 535 GTGTTCTGTGATCGTGTCCATGCTGTGCGCCAGCAGCTGTGCCGACTGCGCAAC 594  
 Db 67 GTGTTCTGTGATCGTGTCTATGTTGTTGCTGTGCGCCAGCAGCTGCCGGAGTGGCGGCG 8  
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RESULT 12  
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 DEFINITION tigr-gss-dog-17000327301868 Dog Library Canis familiaris genomic,  
 genomic survey sequence.  
 ACCESSION CE495701  
 VERSION CE495701.1 GI:36812482  
 KEYWORDS GSS  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 301)  
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun  
 Location/Qualifiers  
 1..301  
 /organism="Canis familiaris"  
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 QY 61 TCGCTGTCCCGGAGCTGTGAAGGACTTCCCGCTGCGCGCGTGAAGCGCGCGCGCG 120  
 Db 158 TCGCTGTCCCGGAGCTGTGAAGGACTTCCCGCTGCGCGCGTGAAGCGCGCGCG 99  
 QY 121 TGGCGCTCCAGCGCGCAGCTGTGCGAGGTGTGCGAGACTTACGACCGGCGCAACGAG 180  
 Db 98 TGGCGCTCCGAGCGCGAGCTGTGCGAGGTGTGCGAGACTTACGACCGGCGCAACGAG 39  
 QY 181 TACTTCTTCACCGGCACTCGGAGGCTTCGGCTTCAT 218  
 Db 38 TACTTCTTCACCGGCACTCGGAGGCTTCGGCTTCAT 1

RESULT 13  
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LOCUS BJ495239 652 bp mRNA linear EST 08-AUG-2002  
 DEFINITION BJ495239 MF01FSA cDNA Oryzias latipes cDNA clone MF01FSA038D18 5', mRNA sequence.  
 ACCESSION BJ495239  
 VERSION BJ495239.1 GI:22147165  
 SOURCE EST.  
 ORGANISM Oryzias latipes (Japanese medaka)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
 REFERENCE 1 (bases 1 to 652)  
 AUTHORS Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.  
 TITLE Medaka EST Project in Takeda's lab  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp.  
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 ORIGIN  
 Query Match 15.7%; Score 200.4; DB 12; Length 652;  
 Best Local Similarity 62.5%; Pred. No. 2.1e-23;  
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 DB 78 GTACTCAATTTGGGGGAACCGGTACGCTTCACTCGTGAGTGATCAAGATTTCCT 137  
 QY 94 CTCGGCGCTGAGCGGCTGACGCTGCGCTCCGAGCGGACGTGCTCGAGGTGTC 153  
 DB 138 CTCGGCGCTGAGCGCTGCTGATGATGCGCAACCGAAGAGGTCTTAGACTGTGT 197  
 QY 154 GACGACTACGACCGGAGCGCAACGAGTACTTTTCGACCGGACCTCGGAGGCTTCGGC 213  
 DB 198 GATGACTATGACCGAGACCGAATGATTTTCTTCGACCGGACGACGACGAGGCTTGTG 257  
 QY 214 TTCACTCTGCTTACGTCGCGGCGGCGGCAAGCTGCGCTTCGCGCGGCGGATGTCGAG 273  
 DB 258 TTCACTAATGTTGACGTTTC---GTCGCGCAAACTCCGATTGTTCTCGAGTGTGTAG 314  
 QY 274 CTCCTCTTCTACAAACGAGATGATCTACTGGGCTCGAGGGCGCGCACTCGAGTACTGC 333  
 DB 315 CTGCTCTTCTACTCAGAAATGCTTTACTGGGCTTGAGAGCGTGCACTCGGACTCTGC 374  
 QY 334 TGCAGCGCGCTCGACGACCGGATGTCGACACCTACACTTCTACTCGGCGGAGGAG 393  
 DB 375 TGTCAAGAACGCTTGAAGATGACGATGTCGATATAGGACTGAGACTCTTTTCGAGGG 434  
 QY 394 CCGGCGCTGTCGGCGCGGAGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 453  
 DB 435 GACATAGTGTTCAGGGGAGGAGGCTGAGACCCGAGAGCTGCGTACACGATTTGG 494  
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 REFERENCE 1 (bases 1 to 505)  
 AUTHORS Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrana, Y., Williams, G. and Brenner, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk  
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DEFINITION mRNA sequence.

ACCESSION BF966122

VERSION BF966122.1 GI:12333337

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)

Homosapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 887)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10040 row: m column: 17

High quality sequence stop: 628.

Location/Qualifiers

## FEATURES

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insert size 2.5 kb and normalized to R0T 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this  
is a NIH\_MGC Library."

## ORIGIN

Query Match 15.2%; Score 193.8; DB 10; Length 887;  
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Job time : 3663 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2004, 11:54:10 ; Search time 5373 Seconds  
(without alignments)

3428.399 Million cell updates/sec

Title: US-10-016-647-2

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Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	2199.5	99.3	1311	9	AB070604 Homo sapi
5	2199.5	99.3	1947	6	AX641934 Sequence
6	2199.5	99.3	1947	9	AF348982 Homo sapi
7	2199.5	99.3	3703	9	AF454548 Homo sapi
8	2122.5	95.8	1744	10	AF454549 Rattus no
9	2120.5	95.7	3323	10	AF454551 Mus muscu
10	2107	95.1	1302	9	AF450110 Homo sapi
11	2107	95.1	1777	10	AF454550 Rattus no
12	2105	95.0	3356	10	AF454552 Mus muscu
13	2105	95.0	5775	6	AX641960 Sequence
14	2076.5	93.7	2235	6	AX478109 Sequence
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20	1108	50.0	268099	2	AC133407 Rattus no
21	1099.5	49.6	209523	10	AC084386 Mus muscu
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 SOURCE  
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 REFERENCE 1  
 AUTHORS Friddle, C.J., Hilbun, E. and Turner, C.A.  
 TITLE Novel human ion channel protein and polynucleotides encoding the same  
 JOURNAL Patent: WO 0250271-A 1 27-JUN-2002;  
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 VERSION AX511262.1 GI:23392139  
 KEYWORDS Homo sapiens (human)  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Friddle, C.J., Hilbun, E. and Turner, C.A.  
 TITLE Novel human ion channel protein and polynucleotides encoding the same  
 JOURNAL Patent: WO 0250271-A 3 27-JUN-2002;  
 FEATURES Lexicon Genetics Incorporated (US)  
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QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
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QY 421 ThrGluPheLeuAsn 425
Db 1717 ACTGAATTCCTGAAT 1731

RESULT 3
AF454547 3670 bp mRNA linear PRI 09-AUG-2002
LOCUS Homo sapiens voltage-gated potassium channel subunit Kv10.1a mRNA,
DEFINITION complete cds, alternatively spliced.
ACCESSION AF454547
VERSION AF454547.1 GI:22164081
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3670)
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium
channel subunits
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3670)
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-2001) Physiology and Neuroscience, New York
University School of Medicine, 550 First Avenue, New York, NY
10016, USA

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polyA_signal
polyA_site
ORIGIN
Alignment Scores:

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Pred. No.: 2,25e-208 Length: 1311  
 Score: 2199.50 Matches: 425  
 Percent Similarity: 97.48% Conservative: 0  
 Best Local Similarity: 97.48% Mismatches: 0  
 Query Match: 99.30% Indels: 11  
 DB: 9 Gaps: 1  
 US-10-016-647-2 (1-425) x AB070604 (1-1311)

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 QY 41 CysArgSerGluArgAspValValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
 DB 121 TGCCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGACGACTACGACCGCGAGCGCAACGAG 180  
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80  
 DB 181 TACTTCTTCGACCGGCATCTCGAGCGCTTCGGCTTCACTCGCTCTACGTGCGCGGCCAC 240  
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
 DB 241 GGCAAGCTGGCTTCGCGCGCGGATGTGCGAGCTCTCTCTACAAAGAGATGATCTAC 300  
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 QY 201 AlaAspAsnArgSerLeuAspAspArgSerArg----- 211  
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 QY 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe 229  
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 ACCESSION AX641934  
 VERSION AX641934.1 GI:28474564  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1  
 SNYDERS, D.J., OTTSCHYTSCH, N., RAES, A. and van Hoorick, D.  
 New heterotetrameric potassium channels and uses thereof  
 Patent: WO 02096944-A 3 05-DEC-2002, and uses thereof  
 Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)

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Alignment Scores:  
 Pred. No.: 3,89e-208 Length: 1947  
 Score: 2199.50 Matches: 425  
 Percent Similarity: 97.48% Conservative: 0  
 Best Local Similarity: 97.48% Mismatches: 0  
 Query Match: 99.30% Indels: 11  
 DB: 6 Gaps: 1  
 US-10-016-647-2 (1-425) x AX641934 (1-1947)

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656	TCGCTGTCGGGAGCTGCTCAAGCACTTCGCGTGGCGCGGTAGCCGCGCTGCACGGC	715
41	CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu	60
716	TGCGCTCCGAGCGGACGCTGCTCGAGGTGTGCACACTACGACCCGAGCGCAACGAG	775
61	TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis	80
776	TACTTTCGACCGGCACCTCGGAGCGCTTCGGCTTCATCTCTGCTCTACGTGGCGGCCAC	835
81	GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr	100
836	GGCAAGCTGGCTTCGCGCGCGGATGTGCAGCTCTCCCTCTCAACACGAGATGATCTAC	895
101	TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAspArgMet	120
896	TGGGGCTTGAGGGCGGCGCACTCGAGTACTGCTGCCAGCGCCGCTCGACGACCGCATG	955
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1256	TCCGGGATAATGTGAAGCTATCTGCATAGTGTGGTTCACTGCGCGAGTGCATCGTAGGTT	1315
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DEFINITION Homo sapiens voltage-gated potassium channel subunit Kv10.1b mRNA, complete cds, alternatively spliced.  
ACCESSION AF454548  
VERSION AF454548.1 GI:22164083  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3703)  
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.  
TITLE Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits  
JOURNAL Unpublished  
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA

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CDS  
polyA\_signal  
polyA\_site  
ORIGIN  
3703

Alignment Scores:  
Pred. No.: 9,44e-208 Length: 3703  
Score: 2199.50 Matches: 425  
Percent Similarity: 97.48% Conservative: 0  
Best Local Similarity: 97.48% Mismatches: 0  
Query Match: 99.30% Indels: 11  
DB: 9 Gaps: 1

US-10-016-647-2 (1-425) x AF454548 (1-3703)  
Qy 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAenValGlyGlyAlaArgTyr 20







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Qy      121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
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Db      698 TTCGAGGAGCGCACCTGCTGCTGCGCGCGAGATCCTGGCGAGCGTGTCTGCTGTTC 757
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Qy      201 AlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTyr 220
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Qy      221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
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Qy      241 ArgProLeuAsnIleAlaPheLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
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Qy      261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
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RESULT 9
LOCUS   AF454551
DEFINITION Mus musculus voltage-gated potassium channel subunit Kv10.1a mRNA, complete cds, alternatively spliced.
ACCESSION AF454551
VERSION   AF454551.1 GI:22164089
KEYWORDS  Mus musculus (house mouse)
SOURCE    Mus musculus
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3323)
AUTHORS  Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE     Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 3323)
AUTHORS  Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE     Direct Submission
JOURNAL   Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA

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ACCESSION AF450110  
VERSION AF450110.1 GI:31295623  
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REFERENCE 1 (bases 1 to 1302)  
AUTHORS Preisig-Muller R., Derst C., Mederos Y Schnitzler, M. and Daut, J.  
TITLE Cloning and characterization of two novel gamma Kv subunits  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1302)  
AUTHORS Preisig-Muller R., Derst C., Mederos Y Schnitzler, M. and Daut, J.  
TITLE Direct Submission  
JOURNAL Submitted (23-NOV-2001) University of Marburg, Institute of  
Physiology, Deutschhausstrasse 1-2, Marburg 35037, Germany  
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Qy 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe 229  
652 TCCGGGATTAATGAAGTATCTGCTAGCTGTTTACCGCGGAGTGTATGTCGGTTC 711  
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VERSION AF454550.1 GI:22164087  
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ORGANISM Rattus norvegicus  
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REFERENCE 1 (bases 1 to 1777)  
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.  
TITLE Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 1777)  
TITLE Vega-Saenz de Miera, E.C. and Rudy, B.  
JOURNAL Direct Submission  
SUBMITTED (04-DEC-2001) Physiology and Neuroscience, New York  
UNIVERSITY School of Medicine, 550 First Avenue, New York, NY  
10016, USA  
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Db 287 TCGCTGTCCCGGAGCTGCTCAAGGACTTCCCGTCCCGCTGTGACCCGCGTGCACGCG 346  
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212	Qy	-----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe	229
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VERSION	AF454552.1				
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ORGANISM	Mus musculus				
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AUTHORS	Vega-Saenz de Miera, E.C. and Rudy, B.				
TITLE	Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3356)				
AUTHORS	Vega-Saenz de Miera, E.C. and Rudy, B.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA				
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330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349  
Db TCTCAGCTCTTGAACATGGGCTGGACCTGGAAACATCCAAAGGATTTCCGCGAGCATC 1348  
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RESULT 13  
AX641960 5775 bp DNA linear PAT 21-FEB-2003  
LOCUS  
DEFINITION Sequence 29 from Patent WO02096944.  
ACCESSION AX641960

AX641960.1 GI:28474590  
Mus musculus (house mouse)  
Mus musculus  
REFERENCE  
1  
AUTHORS  
Snyders,D.J., Otschytch,N., Raes,A. and van Hoorick,D.  
TITLE  
New heterotetrameric potassium channels and uses thereof  
JOURNAL  
Patent: WO 02096944-A 29 05-DEC-2002;  
VIAMs Interuniversitair Instituut voor Biotechnologie vzw. (BE)  
FEATURES  
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Db 3484 TCGCTGTCCCGGAGCTGCTCAAGGACTTCCCGCTCGCGCGCTGAGCGCGCTGCACGGC 3543  
Qy 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
Db 3544 TGGCGCTCGAGCGCGACGCTGCTCGAAGTGTGCGACGACTACGACCGGGAGCGACAGAG 3603  
Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80  
Db 3604 TACTTCTTCGACCGACACTCGGAGGCTTCGGCTTCATCTCTGTGTACGTGCGCGGCAC 3663  
Qy 81 GlyLeuLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
Db 3664 GGGAAAGCTCGCTTCGCGCGCGGATGTGCGAGCTCTCTCTTCTACACGAGATGATCTAC 3723  
Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120  
Db 3724 TGGGCGCTGGAGGCTGGCACCTGGAGTACTGCTGCCAGCGCGCTAGACGACCGCATG 3783  
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
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Qy 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr 160  
Db 3835 CGTCCCGCGGACCGCGCGCGCCCTCCCGCGCTGGCTGGAGCGCATGCGCGCGGAC 3894  
Qy 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPhe 180  
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Db 3955 GTGATCGTGTCCATGCTGTGCGCGCAGCAGCTGCGCGCATGCTGCGCGCGGT 4014  
Qy 201 AlaAspAsnArgSerLeuAspArgSerArg----- 211  
Db 4015 GCTGACAAACCGAGTCTGGATGACCGGAGCAGGTACTCCGCGCGCGCTGGGAGGGAACCC 4074

QY 212 -----IleIleGluAlaIleCysIleGlyTyrPheThrAlaGluCysIleValArgPhe 229  
 Db 4075 TCGGGNATATTGAGCTATCTCATAGGTGTTTACCGGGAGTGCATCTGCGGTTC 4134  
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 QY 250 AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln 269  
 Db 4195 GCAATACGCGCCCTATTACATCTCTGTGCTAATGACAGTGTTCACGGCAGAACTCTCAA 4254  
 QY 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheThrValIle 289  
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 ACCESSION AX478109  
 VERSION AX478109.1 GI:22217069  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Tang, Y.T., Yue, H., Nguyen, D.B., Hafalia, A.J., Elliott, V.S., Lu, Y.,  
 Walla, N.K., Yao, M.G., Baughn, M.R., Gandhi, A.R., Ding, L.,  
 Sanjanwala, M., Rankumar, J., Arvizu, C., Gietzen, K.J., Lai, P.G.,  
 Azimzai, J., Khan, F.A., Thangavelu, K., Thornton, M., Lu, D.A.,  
 Tribouley, C.M., Warren, B.A., Ison, C.H., Das, D., Raumann, B.E.,  
 Policky, J.L. and Kearney, L.  
 TITLE Transporters and ion channels  
 JOURNAL Patent: WO 0240541-A 39 23-MAY-2002;  
 Incyte Genomics, Inc. (US)  
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 Db 488 TCGCTGTCCCGGGAGCTCTGAAGGACTTCCCGTGGCGCGCGGTGAGCGCGCTGCACGGC 547  
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
 Db 548 TCGCGCTCCGAGCGCAGCTGCTCGAGGTGTCGAGACTACGACCGCGAGCGCAACGAG 607  
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 QY 141 ArgProGlyGlyAla-GluAlaAlaProSerArgArgTyrPheLeuGluArgMetArgTh 160  
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 QY 180 eValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAla 200  
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 ACCESSION AX392945  
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 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS  
 Yue, H., Thornton, M., Rankumar, J., Tang, Y. T., Azimzai, Y.,  
 Baughn, M. R., Yang, J., Yao, M. G., Hal, P., Waiia, N. K., Gandhi, A. R.,  
 Hatalia, A. J., Nguyen, D. B., Patterson, C., Elliott, V. S.,  
 Tribouley, C. M., Lu, D. A., Xu, Y., Reddy, R., Hernandez, R.,  
 Borowsky, M. L., Lo, T. P., Lu, Y., Policky, J. L., Greene, B. D.,  
 Sanjanwala, M. S., Raumann, B. E., Burford, N., Ison, C. H., Lee, E. A.,  
 Ding, L., Das, D., Kallick, D. A., Khan, F. A. and Seilhamer, J. J.  
 Patent: WO 0212340-A 47 14-FEB-2002;  
 JOURNAL Location/Qualifiers  
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 Db 850 GAGCTCTGAAGGACTTCCCGCTGGCGCGGTGAGCGGCTGCACGGCTGCCGCTCCGAG 909  
 QY 45 ArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGluTyrPhePheAsp 64  
 Db 910 CGCAGCTGCTCGAGTGTGGCAGCACTACGACCGCGAGCGCAACAGGACTTCTTCGAC 969  
 QY 65 ArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArg 84

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 Db 1006 -----GCGGCTCCCTCCAGCGCTGGCGAGCATGCGCGGAGCCCTTCGAGGAGCCC 1059  
 QY 165 ThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPheValIleValSer 184  
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Thu Oct 7 10:52:18 2004

us-10-016-647-2.rge

Page 16

Search completed: April 19, 2004, 15:30:03  
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GenCore version 5.1.6  
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Maximum Match 100%

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10: geneseqn2004s:\*

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and is derived by analysis of the total score distribution.

SUMMARIES

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5	2199.5	99.3	5174	9 ADD01447	ADD01447 Human TCH
6	2105	95.0	5775	7 AB224716	AB224716 Murine po
7	2095.5	94.6	1651	7 ABX72192	ABX72192 Human NOV
8	2076.5	93.7	2235	6 ABK83228	ABK83228 Human tra

9	1758	79.4	2312	6 AAD33662	AAD33662 Human TRI
10	1410.5	63.7	950	9 ADD01489	ADD01489 Mouse TCH
11	880.5	39.8	1401	2 AAZ23803	AAZ23803 Human Kv6
12	880.5	39.8	1401	5 AAS75631	AAS75631 DNA enco
13	876	39.5	1560	7 AB224710	AB224710 Human pot
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33	687	31.0	2517	3 AAZ51620	AAZ51620 Human mem
34	685.5	30.9	1476	3 AAZ36410	AAZ36410 cDNA enco
35	685.5	30.9	2421	3 AAZ36409	AAZ36409 cDNA enco
36	685	30.9	2293	2 AAZ11899	AAZ11899 Human pot
37	683	30.8	3102	2 AAZ11905	AAZ11905 Human pot
38	683	30.8	5027	6 AB235328	AB235328 Human gen
39	675	30.5	2573	6 ABS67808	ABS67808 Human rec
40	667	30.1	3032	4 ABA09051	ABA09051 Human K c
41	661	29.8	461	6 ABK27494	ABK27494 DNA enco
42	642	29.0	1488	2 AAZ06653	AAZ06653 hkv5.1 hu
43	642	29.0	1880	2 AAZ06652	AAZ06652 hkv5.1 hu
44	636.5	28.7	1248	6 ABK9795	ABK9795 cDNA enco
45	636.5	28.7	1455	7 ABX72191	ABX72191 Human NOV

ALIGNMENTS

RESULT 1

ABN83930

ID ABN83930 standard; cDNA; 1278 BP.

XX ABN83930;

XX AC

DT 06-SEP-2002 (first entry)

XX Human voltage-gated potassium channel-like protein encoding cDNA.

Human; voltage-gated potassium channel; ion channel; neuroprotective;  
therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;  
single nucleotide polymorphism; foetal brain; brain; cerebellum;  
pituitary; prostate; thymus; lymph node; bone marrow; trachea;  
foetal liver; liver; testis; thyroid; salivary gland; stomach;  
skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;  
12 week old embryo; adenocarcinoma; osteosarcoma; Gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1278

FT /product= "voltage-gated potassium channel-like protein"

FT /replace(432,C)

FT /tag= b

FT /standard\_name= "single nucleotide polymorphism"

XX WO200250271-A2.

XX 27-JUN-2002.

XX



KW 12 week old embryo; adenocarcinoma; osteosarcoma; gene; ds.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT 5'UTR 1..456  
 FT CDS /\*tag= a  
 FT /product= "voltage-gated potassium channel-like protein"  
 FT /product= b  
 FT /replace(888,C)  
 FT variation /\*tag= c  
 FT /standard name= "single nucleotide polymorphism"  
 FT 3'UTR 1735..1844  
 FT /\*tag= d  
 XX WO200250271-A2.  
 XX 27-JUN-2002.  
 XX 10-DEC-2001; 2001WO-US048050.  
 XX 20-DEC-2000; 2000US-0257932P.  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX Friddle CJ, Hilbun E, Turner CA;  
 PI WPI; 2002-508799/54.  
 XX P-PSDB; ABB83073.  
 DR Human ion channel polynucleotide useful in therapeutic, diagnostic and  
 PT pharmacogenomic applications.  
 XX  
 PS Disclosure; Page 36; 36pp; English.  
 CC The invention relates to a novel human ion channel polynucleotide that  
 CC shares structural similarity with voltage-gated potassium channel  
 CC proteins. The activity of the protein of the invention may be described  
 CC as neuroprotective. The protein of the invention is useful in  
 CC therapeutic, diagnostic and pharmacogenomic applications, for example to  
 CC identify mutations associated with a particular disease, as a diagnostic  
 CC or prognostic assay, or in gene therapy. The protein of the invention has  
 CC been found to be expressed in human foetal brain, brain, cerebellum,  
 CC pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal  
 CC liver, liver, testis, thyroid, salivary gland, stomach, skeletal muscle,  
 CC heart, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo,  
 CC adenocarcinoma and osteosarcoma cells. The current sequence represents  
 CC the human voltage-gated potassium channel-like protein encoding DNA  
 CC sequence  
 XX  
 SQ Sequence 1844 BP; 314 A; 540 C; 596 G; 394 T; 0 U; 0 Other;  
  
 Alignment Scores:  
 Pred. No.: 4,46e-231 Length: 1844  
 Score: 2215.00 Matches: 425  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
  
 US-10-016-647-2 (1-425) x ABB83931 (1-1844)  
 QY 1 MetThrPheGlyArgSerGlyValAlaSerValValLeuAsnValGlyValArgTyr 20  
 DB 457 ATGACCTTCGGCGCGAGCGGGCGGCTCGGTGTCGTGACGTGGCGCGCGCGGTAT 516  
 QY 21 SerLeuSerArgGluLeuLeuLysPheProLeuArgArgValSerArgLeuHisGly 40  
 DB 517 TCGCTGTCCGGGAGCTGCTGAAGACTTCGCGCTGCGCGCGGTGAGCGGCTGACGGC 576  
 QY 41 CysArgSerGluArgAspValLeuValCysAspAspTyrAspArgGluArgAsnGlu 60

577 TGCCGCTCCGAGCGCGACGCTGCTCGAGGTGTGCGACGACTACGACCGCGAGCGACGAG 636  
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80  
 DB 637 TACTTCTTGACCGGACCTCGGAGGCTTCGGGTTTCATCTCTGCTCTACGTGCGCGCCAC 696  
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetLleTyr 100  
 DB 697 GGCACAGCTGCGCTTCGCGCGGAGTGTGCGAGCTCTCTCTTACACAGAGATGATCTAC 756  
 QY 101 TrpGlyLeuGluGlyAlaHisIleuGluTyrCysGluArgGluArgLeuAspArgMet 120  
 DB 757 TGGGGCTGAGGGCGCGCACCTCGAGTACTGTGTCGAGCGCGCTTCGACGACCGCATG 816  
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
 DB 817 TCCGACACCTACACCTTCTACTCGCGCGAGCGGCGTGTGCGCGCGAGCGGCG 876  
 QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrTrpLeuGluArgMetArgArgThr 160  
 DB 877 CGCCCGCGGGCGGCGGCGCTCCCTCCAGCGCTGCTGGAGCGCATGCGCGCGAGC 936  
 QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPhe 180  
 DB 937 TTCAGAGAGCCACGCTCGTCTGCGCGCGAGATCTCTGGTAGCGTGTCTGTTGTTT 996  
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200  
 DB 997 GTGATCGTGTCCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1056  
 QY 201 AlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTyr 220  
 DB 1057 GCGCAACCGCGAGCTGGATGACCGAGAGATTAATGAAGCTATCTGCAATAGTTGG 1116  
 QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240  
 DB 1117 TTCACGTCCGAGTGCATCGTGAGGTTCAATGTCTCCAAAAACAAGTGTGAGTTTCAAG 1176  
 QY 241 ArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260  
 DB 1177 AGACCCCTGAACATCATTAATTTACTTACGGCAATCACCGCGTATTCATCTCTGTGTGATG 1236  
 QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280  
 DB 1237 ACAGTGTTCACGCGGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGAGGTACTT 1296  
 QY 281 ArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300  
 DB 1297 AGAATCATGAGGATTTTGGGTGATTAAGCTTGCCTGCTCACTTCAATGCTCTCAGACA 1356  
 QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320  
 DB 1357 CTGGTTTGACTCTCAACGTTGCTACCGAGAGATGGTTATGTTACTTCTTCATTTGT 1416  
 QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340  
 DB 1417 GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTCTTCTGAACATGGCTGGACCTGAA 1476  
 QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360  
 DB 1477 ACATCCAAACAGGACTTTACCGACATTCCTGCTGCTGCTGGTGGGTGATTATCTCTATG 1536  
 QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380  
 DB 1537 ACTACAGTTGGCTATGGAGATATGATCTATCAGAGTGCCTCGAAGAATTCCTGGAGGA 1596  
 QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400  
 DB 1597 GTTGTGTGTGTCAGTGGAAATGTTCTATTGGCATTACCTATCATCTTTTATCTACCATAGC 1656  
 QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420  
 DB 1657 TTTGTGACAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCC 1716

QY 421 ThrGluPheLeuAsn 425  
 DB 1717 ACTGAATTCCTGAT 1731

RESULT 3  
 ADD01427  
 ID ADD01427 standard; DNA; 1308 BP.  
 XX AC  
 XX ADD01427;  
 XX DT  
 XX 01-JAN-2004 (first entry)  
 XX Human TCH136 coding sequence.

de; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;  
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
 KW cytotatic; antiasthmatic; antiarthritic; cerebroprotective;  
 KW anti allergic; dermatological; cardiant; antiparkinsonian; neuroleptic;  
 KW glucose transporter; potassium ion channel protein; diabetes;  
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;  
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;  
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;  
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;  
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 1..1308  
 FT CDS

FT /\*tag= a  
 FT /product= "human TCH136 protein"  
 FT /function= "voltage-dependent potassium ion channel"  
 XX  
 PN W02003054190-A1.  
 XX  
 XX 03-JUL-2003.  
 XX  
 XX 19-DEC-2002; 2002WO-JP013290.  
 XX  
 XX 21-DEC-2001; 2001JP-00389361.  
 XX 25-DEC-2001; 2001JP-0032577.  
 XX 26-DEC-2001; 2001JP-00394947.  
 XX 26-DEC-2001; 2001JP-00395467.  
 XX 06-FEB-2002; 2002JP-00030010.  
 XX 08-FEB-2002; 2002JP-00033095.  
 XX 06-JUN-2002; 2002JP-00165336.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Nakanishi A, Sagiya Y, Uno Y;  
 XX WPI; 2003-541817/51.  
 XX P-PSDB; ADD01426.  
 XX  
 XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and  
 PT potassium channel protein TCH136 and DNA encoding them for diagnosis,  
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and  
 PT digestive disorders.  
 XX  
 XX Claim 62; SEQ ID NO 63; 221bp; Japanese.  
 XX  
 XX The invention relates to a novel glucose transporter TCH099, vesicular  
 CC glutamate transporter TCH177 and voltage-dependent potassium ion channel  
 CC protein TCH136. The sequences are useful in the treatment, prevention and  
 CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,  
 CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,  
 CC gastritis, ileitis and rectal inflammation), inflammatory diseases,  
 CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,

CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as  
 CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),  
 CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and  
 CC atopic dermatitis), circulatory disorders (such as heart failure), cancer  
 CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,  
 CC pancreas, bladder, breast, fallopian tubes, or colon), central nervous  
 CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and  
 CC secretory disorders (such as hyperprolactinemia and Cushing's disease). This  
 CC sequence represents the coding sequence for the novel human voltage-gated  
 CC potassium ion channel protein TCH136.

XX SQ Sequence 1308 BP; 238 A; 362 C; 389 G; 319 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,32e-229 Length: 1308  
 Score: 2199.50 Matches: 425  
 Percent Similarity: 97.48% Conservative: 0  
 Best Local Similarity: 97.48% Mismatches: 0  
 Query Match: 99.30% Indels: 11  
 DB: 9 Gaps: 1

US-10-016-647-2 (1-425) x ADD01427 (1-1308)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20  
 DB 1 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGTAACGTGGCGGCGCGGTAT 60  
 QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40  
 DB 61 TCGTGTTCGGCGAGCTGCTGAAGGACTTCCCGCTCGCGCGGTGACCGGC 120  
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
 DB 121 TCGCGCTCCGAGCGCGACGTGCTCGAGGTGTGGCAGCATACGACCGCGCGCACAGAG 180  
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80  
 DB 181 TACTTCTTCACCGGCACCTCGGAGGCTTCGGCTTCATCTCTACGTGCGCGCCAC 240  
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
 DB 241 GGCAAGCTGGCTTCGCGCGCGGATGTGGAGCTCTCTTCTACACGAGATGATCTAC 300  
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120  
 DB 301 TGGGGCTCGAGGGCGCGCACCTCGAGTACTGTCTCGACGCGCGCTCGACGACCGCATG 360  
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
 DB 361 TCCGACACCTACACCTTCTACTCGGCGCAGAGCGGGCGGTGTCTGGCGCGCGCAGAGGG 420  
 QY 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTyrLeuGluArgMetArgArgThr 160  
 DB 421 CGCCCCGGCGGCGCGGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGGACC 480  
 QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180  
 DB 481 TTCAGAGAGCCACGCTGCTGGCGCGCGCAGATCTGGCTAGCGTGTGGTGTGTTC 540  
 QY 181 ValIleValSerMetValValLeuValCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200  
 DB 541 GTGATGTGTTCATGT 600  
 QY 201 AlaAspAsnArgSerLeuAspAspArgSerArg----- 211  
 DB 601 GCGGACAAACGCGAGCTCGATGACCGAGCAGGTACTCCGCGCGCGCTCGGAGGGAGCCC 660  
 QY 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe 229  
 DB 661 TCGGGGATAATTGAAGTATCTCATAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720  
 QY 230 IleValSerIleAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeu 249

Db 721 ATTGCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTG 780  
 Qy 250 AlalleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln 269  
 Db 781 GCAATCACCCCGATTATACATCTCTGTGTGATGACAGTGTTTACAGGCGAGAACTCTCAA 840  
 Qy 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle 289  
 Db 841 CTCCAGAGCGCTGGAGTCACCTTGAGGTACTTGAATGATGAGGATTTTGGGTGATT 900  
 Qy 290 LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr 309  
 Db 901 AGCTTCCCGCCACCTTCACTTGGTCTTCAGACACCTGGTTTCACTCTCAACGTTGCTAC 960  
 Qy 310 ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu 329  
 Db 961 CGAGAGATGGTTATGTACTTCTCTTCACTTGTGTTGCCATGCAATCTTTAGTGCATT 1020  
 Qy 330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349  
 Db 1021 TCTCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCAAACAGGACTTTACCAAGCAT 1080  
 Qy 350 ProAlaAlaCysTrpIleValIleIleSerMetThrValGlyTyrGlyAspMetTyr 369  
 Db 1081 CTGTGCTGCTGCTGGTGGTGTATTATCTATGACTACAGTTGGCTATGGAGATATGAT 1140  
 Qy 370 ProlleThrValProGlyArgIleLeuGlyValCysValValSerGlyIleValLeu 389  
 Db 1141 CCTATCACAGTCCCTGGAAGAATCTTGGAGGAGTTTGTGTGTCAGTGAATTTCTCTA 1200  
 Qy 390 LeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409  
 Db 1201 TTGGCATTACCTTATCTATCTACCATAGCTTTGTGCACTGTATCATGAGCTCAAG 1260  
 Qy 410 PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425  
 Db 1261 TTTAGATCTGTAGGTATAGTAGGACCTCTCCACTGAATTCCTGAAT 1308  
 RESULT 4  
 ABZ24711  
 ID ABZ24711 standard; cDNA; 1947 BP.  
 XX AC ABZ24711;  
 XX DT 07-APR-2003 (first entry)  
 XX DE Human potassium channel subunit Kv10.1 cDNA.  
 XX KW Potassium channel; Kv10.1; human; anticonvulsant; antiarrhythmic;  
 KW tranquilizer; cytostatic; virucide; nootropic; neuroprotective;  
 KW epilepsy; long QT syndrome; muscular ataxia; arrhythmia; gene therapy;  
 KW chromosome 2p21; gene; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX CDS 596..1906  
 XX FT /\*tag= a  
 XX FT /note= "Human Kv10.1"  
 XX FN WO200296944-A2.  
 XX PD 05-DEC-2002.  
 XX PF 31-MAY-2002; 2002WO-BP006082.  
 XX PR 31-MAY-2001; 2001EP-00202060.  
 XX PA (VLA-- ) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 XX PI Snyders DJ, Ottschysch N, Raes A, Van Hoorick D;  
 XX WPI; 2003-140443/13.

P-PSDB; ABP58352.  
 Novel voltage-gated heterotetrameric potassium channel useful for  
 diagnosing, preventing and/or treating excitability disorders, comprises  
 Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.  
 Claim 3; Page 50-53; 93pp; English.  
 The present sequence is that of cDNA encoding human potassium channel  
 subunit Kv10.1. The cDNA was obtained by PCR from a brain library. The  
 invention relates to the cloning and characterisation of 3 novel voltage-  
 gated potassium channel subunits that were identified in the human  
 genome: Kv6.3 (located at 16q24.1), Kv10.1 (2p21) and Kv11.1 (9p24.2).  
 Yeast two-hybrid and co-immunoprecipitation experiments showed that these  
 subunits do not form homotetrameric channels, but do form  
 heterotetrameric channels with Kv2.1, Kv3.1 and/or Kv5.1. Co-expression  
 of each of the novel subunits with Kv2.1, Kv3.1 and/or Kv5.1 results in  
 currents that differ from typical Kv2.1 currents. Kv6.3, Kv10.1 and  
 Kv11.1 alone do not reach the plasma membrane but are retained in the  
 endoplasmic reticulum. Co-expression with Kv2.1 results in transport to  
 the plasma membrane. The invention provides novel, voltage-gated  
 heterotetrameric potassium channels comprising Kv2.1, Kv3.1, Kv5.1,  
 Kv6.3, Kv10.1 or Kv11.1. These are useful for identifying a molecule that  
 increases or decreases ion flux through the potassium channel. Nucleic  
 acids encoding the heterotetrameric potassium channels are used in gene  
 therapy to prevent or treat congenital or acquired excitability disorders  
 including epilepsy, long QT syndrome, muscular ataxia, arrhythmia (all  
 claimed), as well as hyperactivity disorders, mental disorders, mood  
 disorders, behavioural disorders, anxiety disorders, hypokalaemic  
 periodic paralysis, spasticity disorders, myotonia and paramyotonia. The  
 nucleic acids can be used to transfect cells. For example, stem cells are  
 used in ex vivo procedures for cell transfection and gene therapy. The  
 nucleic acids are also useful in diagnosis, and in the creation of  
 transgenic or knockout animals  
 SQ Sequence 1947 BP; 324 A; 596 C; 644 G; 383 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,37e-229 Length: 1947  
 Score: 2199.50 Matches: 425  
 Percent Similarity: 97.48% Conservative: 0  
 Best Local Similarity: 97.48% Mismatches: 0  
 Query Match: 99.30% Indels: 11  
 DB: 7 Gaps: 1  
 US-10-016-647-2 (1-425) x ABZ24711 (1-1947)  
 Qy 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20  
 Db 596 ATGACCTTCGGCGCGCAGCGGGCGCTCGTGTGTGTGAACGTGGCGCGCGCGGTAT 655  
 Qy 21 SerLeuSerArgGluLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40  
 Db 656 TCGCTGTCCCGGAGCTGCTCAAGGACTTCCCGTGGCGCGCGTGGCCGCGTGCACGC 715  
 Qy 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
 Db 716 TGGCGCTCCGAGCGCGACGTGCTCGAGTGTGCGACGACTACGACCGGAGCGACGAG 775  
 Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80  
 Db 776 TACTTCTTCGACCGGCGACCTCGAGGCGCTTCGGTTCATCTCTGCTCTACGTGGCGGCGAC 835  
 Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
 Db 836 GGCAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTAC 895  
 Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120  
 Db 896 TGGGCGCTGGAGCGCGCGACCTCGAGTACTGTGTCGAGCGCGCGCTCGACGACCGCATG 955  
 Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140

Db 956 TCCGACACCTTACCTTCTACTCGCGCGAGCGCGCGGTCTCGCGCGCGAGCGG 1015  
 Qy 141 ArgProGlyValAlaGluAlaAlaProSerArgArgTrrLeuGluArgMetArgArgThr 160  
 Db 1016 CGCCCG 1075  
 Qy 161 PheGluGluProThrSerSerLeuAlaAlaGlnLeuAlaSerValSerValValPhe 180  
 Db 1076 TTCAGGAGGCCACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1135  
 Qy 181 ValLeuValSerMetValValLeuValCysAlaSerThrLeuProAspProArgAsnAla 200  
 Db 1136 GTGATGTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1195  
 Qy 201 AlaAspAsnArgSerLeuAspArgSerArg----- 211  
 Db 1196 GCCGACAAACCGAGCTGGATGACCGGAGCAGGTACTCCGCGCGCGCTGGAGGAGCGCC 1255  
 Qy 212 -----IleIleGluAlaIleCysIleGlyTrrPheThrAlaGluCysIleValArgPhe 229  
 Db 1256 TCCGGGATTAATGAAGCTATCTCATAGTGTGTCCTGCGAGTGCATCTGAGGTTC 1315  
 Qy 230 IleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeu 249  
 Db 1316 ATTGTCTCCAAACAAAGTGTGAGTTGTCAAGAGACCCCTGAACATCATTTACTTCTG 1375  
 Qy 250 AlaIleThrProTyrTrrIleSerValLeuMetThrValPheThrClyGluAsnSerGln 269  
 Db 1376 GCAATCAGCGCGTATTACATCTCTGTGTGATGACAGTGTTTACAGGCGAGAACTCTCAA 1435  
 Qy 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle 289  
 Db 1436 CTCAGAGGCTGGAGTACCTTGAGGGTACTTAGAATGATGAGGATTTTGGGTGATT 1495  
 Qy 290 LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr 309  
 Db 1496 AAGCTTGCCCGTCACTTCATTTGCTTCAGACACTCGGTTTGACTCTCAAAAGTTGCTAC 1555  
 Qy 310 ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu 329  
 Db 1556 CGAGAGATGTTATGTTACTTGTCTTCTTCTTGTGTCCTGCTGCTGCTGCTGCTGCT 1615  
 Qy 330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349  
 Db 1616 TCTCAGCTTCTTCAACATGGCTGGAGCTTGGAGAACTCAACAGAGACTTTTACAGCAT 1675  
 Qy 350 ProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTrrClyAspMetTyr 369  
 Db 1676 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1735  
 Qy 370 ProIleThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeu 389  
 Db 1736 CCTATCACAGTGCCTGGAAGATTTCTGGAGGAGTTTGTGTGTGTCAGTGAATTTGTTCTA 1795  
 Qy 390 LeuAlaLeuProIleThrPheIleTrrHisSerPheValGlnCysTrrHisGluLeuLys 409  
 Db 1796 TTGGCATTAACCTATCACTTTTATCTACCATAGCTTTTGTGCTGCTGCTATCATGAGTCAAG 1855  
 Qy 410 PheArgSerAlaArgTrrSerArgSerLeuSerThrGluPheLeuAsn 425  
 Db 1856 TTTAGATCTGCTAGGTATAGTAGAGCCCTCTCCACTGAATTTCTGAT 1903

RESULT 5  
 ADD01447  
 ID ADD01447 standard; cDNA; 5174 BP.

XX AC ADD01447;  
 XX DT 01-JAN-2004 (first entry)  
 XX DE Human TCH136 cDNA sequence.  
 XX KW ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;

KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
 KW cytoskeletal; antiarthritic; cerebrotective;  
 KW antiasthmatic; cardiasthmatic; cardiasthmatic; neuroleptic;  
 KW glucose transporter; potassium ion channel protein; diabetes;  
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;  
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;  
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;  
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;  
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.

XX Homo sapiens.  
 OS  
 XX WO2003054190-A1.  
 PN  
 XX 03-JUL-2003.  
 PD  
 XX 19-DEC-2002; 2002WO-JP013290.  
 PF  
 XX 21-DEC-2001; 2001JP-00389361.  
 PR 25-DEC-2001; 2001JP-00392577.  
 PR 26-DEC-2001; 2001JP-00394947.  
 PR 26-DEC-2001; 2001JP-00395467.  
 PR 06-FEB-2002; 2002JP-00030010.  
 PR 08-FEB-2002; 2002JP-00033095.  
 PR 06-JUN-2002; 2002JP-00165336.  
 XX (TAKE ) TAKEDA CHEM IND LTD.

FA Nakanishi A, Sagiya Y, Uno Y;  
 PI WPI; 2003-541817/51.

XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and potassium channel protein TCH136 and DNA encoding them for diagnosis, treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and digestive disorders.

PS Claim 62; SEQ ID NO 83; 221bp; Japanese.

XX The invention relates to a novel glucose transporter TCH099, vesicular glutamate transporter TCH177 and voltage-dependent potassium ion channel protein TCH136. The sequences are useful in the treatment, prevention and diagnosis of a broad range of diseases including diabetes, hyperlipemia, arteriosclerosis, digestive disorders (such as Crohn's disease, colitis, gastritis, ileitis and rectal inflammation), inflammatory diseases, sepsis, prostatic hypertrophy, reproductive disorders, pneumonia, meningitis, hepatitis, myocarditis, asthma, immune disorders (such as multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus), allergies (such as hay fever, allergic rhinitis, anaphylactic shock and atopic dermatitis), circulatory disorders (such as heart failure), cancer (such as cancer of the lung, kidney, liver, ovary, prostate, stomach, pancreas, bladder, breast, fallopian tubes or colon), central nervous system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and secretory disorders (such as hyperprolactinemia and Cushing's disease). This sequence represents the cDNA sequence for the novel human voltage-gated potassium ion channel protein TCH136.

XX Sequence 5174 BP; 1335 A; 1139 C; 1257 G; 1443 T; 0 U; 0 Other;

Alignment Scores:

Fred. NO.:	1.01e-228	Length:	5174
Score:	2199.50	Matches:	425
Percent Similarity:	97.48%	Conservative:	0
Best Local Similarity:	97.48%	Mismatches:	0
Query Match:	99.30%	Indels:	11
DB:	9	Gaps:	1

US-10-016-647-2 (1-425) x ADD01447 (1-5174)



Qy	1	MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr	20
Db	485	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGCTGAACGTGGCGCGCGCCGGTAT	544
Qy	21	SerLeuSerArgGluLeuLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly	40
Db	545	TGGTGTCCGGAGAGCTGCTGAAGACTTCCCGCTGGCGCGTGAGCCGGCTGCACGGC	604
Qy	41	CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu	60
Db	605	TGCGCGCTCCAGCGCGCAGCTGCTCGAGGTGTGCAGACTACGACCGCGAGCGCAACGAG	664
Qy	61	TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis	80
Db	665	TACTTCTCGACCGGCACTCGAGGCTTCGGCTTCATCTGCTCTACGTGCGCGGCAC	724
Qy	81	GlyLysLeuArgPheAlaProArgMetCysIleLeuSerPheTyrAsnGluMetIleTyr	100
Db	725	GGCAAGCTGGCGTTCGGCGCGCGGATGTGGAGACTCCCTCTCAACACGAGATGATCTAC	784
Qy	101	TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAspArgMet	120
Db	785	TGGGGCTTGAGGGCGGCGACCTCGAGTACTGCTGCCAGCGCGCCCTCGACACCGCATG	844
Qy	121	SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla	140
Db	845	TCCGACACCTACACTTCTACTCGCGCGACGAGCGGGCGGTGCTGGCGCGACGAGCGG	904
Qy	141	ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr	160
Db	905	CGCCCCGGCGGGCGGAGGGCGCTCCCTCCAGCGCGTGGCTGAGCGCATGCGCGCGAC	964
Qy	161	PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPhe	180
Db	965	TTGAGAGAGCCACGTCGTCGCTGGCGCGCAGATCCTGGCTACGCTGTCGGTGTGTT	1024
Qy	181	ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla	200
Db	1025	GTGATCGTGTCCATGGTGGTGCTGTGGCGCAGCACGTTGCCGCACTGGCGCAACGAC	1084
Qy	201	AlaAspAsnArgSerLeuAspAspArgSerArg-----	211
Db	1085	GCGACAAACCGCACCTGGATGACCGAGCAGGTACTCCGCGCGCCCTGGAGGGAGCGCC	1144
Qy	212	-----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe	229
Db	1145	TCCGGGATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTAGGTT	1204
Qy	230	IleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeu	249
Db	1205	ATTCTCTCCAAAAACAAGTGTGATTTGTCAAGAGACCCCTGGAACATCATTTGATTACT	1264
Qy	250	AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln	269
Db	1265	GCAATCAGCGGTATTACATCTCTGTGTGATGACAGTGTTCAGCGCAGAACTCTCAA	1324
Qy	270	LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle	289
Db	1325	CTCAGAGGGCTGGAGTCACCTTCAGGGTACTTAGAATGATGAGGATTTTGGGTGATT	1384
Qy	290	LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr	309
Db	1385	AAGCTTGCCCGTCACTTCATTGGTCTTCAGACACTCGGTTTGACTCTCAACAGTTGCTAC	1444
Qy	310	ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu	329
Db	1445	CGAGAGATGGTTATGTGTACTTGTCTTCATTTGCTTGCATGGCAACTCTTTAGTGCACT	1504
Qy	330	SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle	349
Db	1505	TCTCAGCTTCTTGAACATGGGCTCGACTGGAAACATCCAAACAGGACTTTTACCAGATT	1564
Qy	350	ProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyr	369

Db	1565	CCTGCTCCCTGCCTGGTGGG	GATTATCTCTATGACTACAGTTGCTATGAGATATGAT	1624
Qy	370	ProileThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleVal	leu 389	
Db	1625	CCTATCACAGTGCCTGGAAGAA	TTCTTTGGAGGAGTTTGTTGTGCTGGAATTGTTCTA	1694
Qy	390	LeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu	Iys 409	
Db	1685	TTGGCAATTACCTATCACTTTTATCTACATAGCTTTGTGCAGTGTATATCATGAGCTCAAG	1744	
Qy	410	PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn	425	
Db	1745	TTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAATTCCTGAAT	1792	
RESULT 6				
ABZ24716	ID	ABZ24716	standard; cDNA; 5775 BP.	
XX	AC	ABZ24716;		
XX	DT	07-APR-2003	(first entry)	
XX	DE	Murine potassium channel subunit Kv10.1 - flag sequence.		
XX	KW	Potassium channel; Kv10.1; mouse; transgenic mouse; gene; ss.		
XX	OS	Mus musculus.		
XX	FH	Key	Location/Qualifiers	
FT	misc_feature	3424..4749		
FT	FT	/*tag= a		
XX	XX	/note= "flag"		
XX	PN	W0200296944-A2.		
XX	PD	05-DEC-2002.		
XX	PF	31-MAY-2002; 2002WO-EP006082.		
XX	PR	31-MAY-2001; 2001EP-00202060.		
XX	PA	(VLAA-) VLAAVS INTERUNIVERSITAIR INST BIOTECHNOG.		
XX	PI	Snyders DJ, Ottschytch N, Raes A, Van Hoorick D;		
XX	DR	WPI; 2003-140443/13.		
XX	PT	Novel voltage-gated heterotetrameric potassium channel useful for		
FT	FT	diagnosing, preventing and/or treating excitability disorders, comprises		
XX	XX	Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.		
XX	PS	Example; Page 80-82; 93pp; English.		
XX	CC	The present sequence is that of a construct used in the creation of a		
CC	CC	potassium channel subunit Kv10.1 transgenic mouse. In an example from the		
CC	CC	invention, the construct was microinjected into the pronucleus of a one-		
CC	CC	cell embryo, and then incubated in a foster mother of the FVB/Nico mouse		
CC	CC	strain. The invention provides novel, voltage-gated heterotetrameric		
CC	CC	potassium channels comprising Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or		
CC	CC	Kv11.1. These are useful for identifying a molecule that increases or		
CC	CC	decreases ion flux through the potassium channel (claimed). Nucleic acids		
CC	CC	encoding the heterotetrameric potassium channels are used in gene therapy		
CC	CC	to prevent or treat congenital or acquired excitability disorders		
CC	CC	including epilepsy, long QT syndrome, muscular ataxia, and arrhythmia		
XX	XX			
SO	Sequence	5775 BP; 1327 A; 1530 C; 1532 G; 1386 T; 0 U; 0 Other;		
Alignment Scores:				
Fred. No.:	2.42e-218	Length:	5775	
Score:	2105.00	Matches:	408	
Percent Similarity:	94.72%	Conservative:	5	

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Best Local Similarity: 93.58%
Query Match: 95.03%
DB: 7
Mismatches: 9
Indels: 14
Gaps: 2

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US-10-016-647-2 (1-425) X ABZ24716 (1-5775)

QY	1	MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr	20
Db	3424	ATGACCTTCGGGGCGCGCGGGCGGCTCGGTGGTGTGTGAACGTGGGCGCGCGCGGTAC	3483
QY	21	SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly	40
Db	3484	TCGCTGTCCGGGAGCTGCTCAGGACCTTCCGCTGGCGCGCTGAGCCGGCTGCACGGC	3543
QY	41	CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu	60
Db	3544	TGCGCGTTCGAGAGCGGACAGTGTCTCGAAGTGTGGCGACACTACGACCGGGAGCGCAACGAG	3603
QY	61	TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis	80
Db	3604	TACTTCTTCACCGCACACTCGGAGGCCCTTGGGCTTCATCTGTGTACGTGGCGGCCAC	3663
QY	81	GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr	100
Db	3664	GGGAAGCTGGGCTTCGCGCGCGGATGTGGAGCTCTCTCTTCTACACGAGATGATCTAC	3723
QY	101	TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAspArgMet	120
Db	3724	TGGGGCTTGAGGGTGGCGACCTTGGAGTACTGTGCCAGCGCGCTTAGACGACCGCATTG	3783
QY	121	SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspAlaAla	140
Db	3784	TCGCGACACCCACACCTTTCACGGCGGACAGCGAG-----CTGGCGCGCGAGCAGCCCT	3834
QY	141	ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr	160
Db	3835	CGTCCCGCGGACCCGAGGCGGCGCCCTCCGCGCGCTGGCTGGAGCGCATTCGCGCGGACC	3894
QY	161	PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValAlaPhe	180
Db	3895	TTCCAGAGAGCCACGCTCGTGGCTGGCGCGCGACATCTCGGCCAGCGTGTCCGTGGTGTTC	3954
QY	181	ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla	200
Db	3955	GTGATCGTTCATGGTGGTGTGTGGCGCGACACGCTGCCACCTGCCACTGGCGTGC	4014
QY	201	AlaAspAsnArgSerLeuAspAspArgSerArg-----	211
Db	4015	GCGTACAAACCGCAGTCTGGATGACCGGAGCAGGTACTCCGCCAGCCCTGGGAGGGGAACCC	4074
QY	212	-----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe	229
Db	4075	TCCGGGATAATTGAAGCTATCTGCATAGGTGGTTCACCGCGAGTGCATCTGTGGCGTTC	4134
QY	230	IleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeu	249
Db	4135	ATCGTCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAAACATCATTGACTTACTG	4194
QY	250	AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln	269
Db	4195	GCAATCAGCGCCCTATTACATCTCTGTGCTAATGACAGTGTTTACGCGAGAACTCTCAA	4254
QY	270	LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle	289
Db	4255	CTCCAGAGGCTGGGCTCACCTTGGGGTCTCTCCGAATGATGGGATCTTCTGGGTGATC	4314
QY	290	LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr	309
Db	4315	AAGCTTGC CGGCACTTCATGTGTCTGCACAGCACTGGGCTTGTACTCTCAAGCGATGCTAC	4374
QY	310	ArgGluMetValMetLeuLeuValPheIleCysValAlaAlaMetAlaIlePheSerAlaLeu	329
Db	4375	CGAGAGATGGCTATGTACTTGTCTTCATCTGTGTGCATGGCACTCTTTAGTGACCTC	4434

	Qy	330	SerClnLeuLeuCuhSiGlyIleAspLeuGluThrSerAsnLysAepPheThrSerIle	349
	Dd	4435	TTCAGCTCCCTGGACATCGGCCTGGACC <sup>*</sup> GGAACAATCCAACAGGANTTTGCCAGCATC	4494
	Qy	350	ProAlaalaCysTrpTrpValIlelleSerMetThrThrValGlyTyrGlyAspMetTyr	369
	Dd	4495	CCGCGTCGCCGTGGTGGGTGATTATCTCATGACTACAGTTGGCTAIGAGATAITGAT	4554
	Qy	370	ProIlethrValProGlyArgIleLeuGlyGlyValCysValvalSerGlyIleValLeu	389
	Dd	4555	CCTATCACGGTGCTCGGAAGAATCTTGGAGGAGTTGTGTTGTCTCATGGGATTTGTCG	4614
	Qy	390	LeuAlaLeuProIlethrPheIleTyrHisSerPheValcInCystYrHisGluLeuLys	409
	Dd	4615	TTGGCAATTACCCATCACTTTCACTCTACATAGCTTTGTGCAGTGCTACCAACAGAGCTCAAG	4674
	Qy	410	PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn	425
	Dd	4675	TTTAGATTCGGCTAGATATAGTAGAGCCTCTCAGCTGAGTTCCTCGAAT	4722

RESIST 7

RESULT /  
ABX72192  
ID ABX72192 standard: CDNA: 1651 BP.

AC ABX72192;

DT 03-JUN-2003 (first entry)

Human NOVX polynucleotide #23.

XX Human, NOVX: gene, ss, metabolic disorder; cardiomyopathy; diabetes; ASD  
 XX hypertension; congenital defect; aortic stenosis; valve disease;  
 KW aortic stenosis; ventricular; canal defect; ductus arteriosus;  
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;  
 KW Pyloric stenosis; scleroderma; atherosclerosis; infectious disease;  
 KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;  
 KW Parkinson's disease; immune disorder; haematopoietic disorder;  
 KW hemophilia; hypercoagulation; Crb3n's disease; cancer.

XX Homo sapiens.

XX  
PN  
W0200281498-A2XX  
17-0000-2002

03-APR-2003 2003WQ-IIS010780

XX	03-APR-2001	2001US-0281086P	PR
	03-APR-2001	2001US-0281136P	PR
	05-APR-2001	2001US-0281863P	PR
	05-APR-2001	2001US-0281906P	PR
	06-APR-2001	2001US-0282020P	PR
	10-APR-2001	2001US-0282930P	PR
	12-APR-2001	2001US-0282934P	PR
	12-APR-2001	2001US-0283512P	PR
	13-APR-2001	2001US-0283710P	PR
	17-APR-2001	2001US-0284234P	PR
	17-APR-2001	2001US-0285325P	PR
	20-APR-2001	2001US-0285381P	PR
	20-APR-2001	2001US-0285609P	PR
	23-APR-2001	2001US-0285748P	PR
	23-APR-2001	2001US-0285890P	PR
	24-APR-2001	2001US-0286068P	PR
	25-APR-2001	2001US-0286292P	PR
	27-APR-2001	2001US-0287213P	PR
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	30-MAY-2001	2001US-0294484P	PR
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	19-JUN-2001	2001US-0295237P	PR
	19-JUN-2001	2001US-0295276P	PR
	12-SEP-2001	2001US-0281750P	PR

25-SEP-2001; 2001US-0324800P.  
 25-SEP-2001; 2001US-0324802P.  
 27-SEP-2001; 2001US-0325684P.  
 17-OCT-2001; 2001US-0330143P.  
 14-NOV-2001; 2001US-0332131P.  
 14-NOV-2001; 2001US-0332240P.  
 14-NOV-2001; 2001US-0332779P.  
 21-NOV-2001; 2001US-0332115P.  
 04-DEC-2001; 2001US-0337621P.  
 03-JAN-2002; 2002US-0345783P.  
 16-JAN-2002; 2002US-0350251P.  
 02-APR-2002; 2002US-00114270.  
 (CURA-) CURAGEN CORP.  
 Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA,  
 Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD;  
 Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;  
 Padigaru M, Shinkets RA, Gangoli EA, Taupier RJ, Casman SJ, Ji W;  
 Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;  
 MacDougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;  
 Ellerman K;  
 WPI; 2003-046858/04.  
 P-PSDB; ABUS4564.  
 New isolated NOVX polypeptide useful for treating atherosclerosis,  
 metabolic disorders, diabetes, obesity, infectious disease, anorexia,  
 neurodegenerative disorders, Alzheimer's disease and cancer.  
 Claim 17; Page 136; 666pp; English.  
 The invention relates to human polypeptides, termed NOVX, and the  
 polynucleotides encoding them. The polypeptides and polynucleotides are  
 useful for diagnosing disease, and screening for potential therapeutic  
 agents. The sequences are useful for treating metabolic disorders,  
 cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic  
 stenosis, atrial septal defect (ASD), atrioventricular canal defect,  
 ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular  
 septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,  
 atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative  
 disorders, Alzheimer's disease, Parkinson's disease, immune disorders,  
 haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease  
 and cancer. Sequences ABX72170-ABX72275 represent human NOVX  
 polynucleotides of the invention  
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 Pred. No.: 4,11e-218 Length: 1651  
 Score: 2095.50 Matches: 411  
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 Best Local Similarity: 91.54% Mismatches: 3  
 Query Match: 94.60% Indels: 35  
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 US-10-016-647-2 (1-425) x ABX72192 (1-1651)  
 QY 1 MetThrPheGlyArgSerGlyValAlaSerValValLeuAsnValGlyGlyValArgTyr 20  
 DB 58 ATGACCTTCGGCGGAGCGGGCGGCGCTCGGTGGTGTGACGTGGCGGCGCGGAT 117  
 QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40  
 DB 118 TCGCTGTCCCGGAGCTGTGAAGACATCCCGCTGCCGCGGTGAGCGCGTGCACGCG 177  
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
 DB 178 TCCCGCTCCGACGGAGCGTGTCTGAGGTGTGCGACGACTACGACCGGAGCGAAGAG 237  
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80  
 DB 238 TACTTCTTCGACCGGCACTTCGAGAGGCTTCGGCTTCATCCCTGCTCTAGTGGCGGCGCC 297

QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetLeuTyr 100  
 DB 298 GGCAGCTCGCTTCGGCGCGGAGTGTGCGAGCTCTCTTCTACCAACGAGATGATCTAC 357  
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAspArgMet 120  
 DB 358 TGGGGCTTGGAGGGCGCGCACCTCGAGTACTGTGCGACGCGCGCTCGACACCGCATG 417  
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
 DB 418 TCGGCACTACACCTTCTACTCGGCGGAGCGGGCGTGTCTGGCGCGCGACGAGGCG 477  
 QY 141 ArgProGly-----GlyAlaGluAlaAlaPro--- 149  
 DB 478 CGCCCCGGCGCGAGCGCGCTCCCTCCAGGCGCTGGCTGGAGCGCATCGCGGCGACCTT 537  
 QY 150 -----SerArgArgTyrTrpLeuGluArgMetArgArgThrPhe 161  
 DB 538 CGAGGAGCCACGCTCGCTCGCTGGCGCGAGCGCTGGCTGGAGCGCATCGCGGCGACCTT 597  
 QY 162 GluGluProThrSerSerLeuAlaAlaGlnLeuLeuAlaSerValSerValValPheVal 181  
 DB 598 GAGGAGCCACGCTCGCTCGCTGGCGCGAGATCTCGCTAGCGTGTCTGGTGTGTTCGTG 657  
 QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAla 201  
 DB 658 ATCGTGTCCATGTGTGTGTGCGCGCAGACGCTTCCCGACCTGGCGCAACGCGAGCGCC 717  
 QY 202 AspAsnArgSerLeuAspArgSer----- 210  
 DB 718 GACAAACCGGAGCGCTGATGACCGAGCAGTACTCCGCGCGCGCTGGAGGCGCGCTCC 777  
 QY 211 -----ArgIleLeuGluAlaAlaCysIleGlyTrpPheThrAlaGluCys 225  
 DB 778 GGTGTCTTCTTGACAGGATAATGAAGCTATCTGCATAGTGTGTCTACGCGGAGTGC 837  
 QY 226 IleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIle 245  
 DB 838 ATCGTGGGTTCATTGTCTCCAAACAAAGTGTGAGTGTTCAGAGACCCCTGAACATC 897  
 QY 246 IleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGly 265  
 DB 898 ATTGATTTACTGCAATACGCGCTATTACATCTCTGTGTGATGACAGTGTTCAGGC 957  
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 DB 958 GAGAACTCTCACTCCAGAGGCTGGAGTCACCTTGAGGGTACTTAGAATGATGAGGATT 1017  
 QY 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeu 305  
 DB 1018 TTTTGGGTGATTAAGCTTGGCGCTCACTTCATTGGTCTTCAGACACCTCGGTTTGACTCTC 1077  
 QY 306 LysArgCysTyrArgGluMetValMetLeuValPheIleCysValAlaMetAlaIle 325  
 DB 1078 AAACGTGTCTACGAGAGATGGTATGTACTTGTCTTCAITTTGTGTGCGATGCGAATC 1137  
 QY 326 PheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345  
 DB 1138 TTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGAC 1197  
 QY 346 PheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyr 365  
 DB 1198 TTTACAGCATTCCTGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTTGGCTAT 1257  
 QY 366 GlyAspMetTyrProIleThrValProGlyValGlyIleLeuGlyValCysValValSer 385  
 DB 1258 GGAGATATGATCTATCAGTGCCTGGAGAAATCTTGGAGAGATTGTGTGTGTCAGT 1317  
 QY 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405  
 DB 1318 GGAATTTCTTATTTGGCATTACCTATCATTCTTATCTACCATAGCTTTGTGCGATGTTAT 1377

QY 406 HisGluLeuLysPheArgSerAlaArg 414  
 DB 1378 CATGAGCTCAGTTTAGACTGCTAGG 1404

RESULT 8  
 ABK83228  
 ID ABK83228 standard; cDNA; 2235 BP.  
 XX  
 AC ABK83228;  
 CC  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human transporter and ion channel, TRICH19, Incyte ID 7492060CB1, cDNA.  
 XX  
 KW Human; ss; gene; transporter and ion channel; TRICH; transport disorder;  
 KW neurological disorder; muscle disorder; immunological disorder; cancer;  
 KW scleroderma; systemic lupus erythematosus; allergy; leukaemia;  
 KW cell proliferative disorder; cervical cancer; breast cancer;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW myotonic dystrophy; catatonia; endocrine disorder; diabetes;  
 KW Grave's disease; gastrointestinal disorder; Crohn's disease;  
 KW renal disorder; Good pasture's syndrome; viral infection; cirrhosis;  
 KW bacterial infection; fungal infection; parasitic infection;  
 KW protozoal infection; helminthic infection; cardiovascular disorder;  
 KW atherosclerosis; hepatic disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200240541-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 25-OCT-2001; 2001WO-US046055.  
 XX  
 PR 27-OCT-2000; 2000US-0243989P.  
 PR 03-NOV-2000; 2000US-0245904P.  
 PR 09-NOV-2000; 2000US-0247673P.  
 PR 17-NOV-2000; 2000US-0249661P.  
 PR 20-NOV-2000; 2000US-0252323P.  
 PR 01-DEC-2000; 2000US-0250790P.  
 XX  
 PA (INCYTE) INCYTE GENOMICS INC.  
 XX  
 PI Tang YT, Yue H, Nguyen DB, Hafalia AJA, Elliott VS, Lu Y;  
 PI Wallia NK, Yao MG, Baughn MR, Gandhi AP, Ding L, Sanjanwala M;  
 PI Ramkumar J, Arvizu C, Gietzen KJ, Lal PG, Azimzai Y, Khan PA;  
 PI Thangavelu K, Thornton M, Lu DAM, Tribouley CM, Warren BA, Ison CH;  
 PI Das D, Raumann BS, Policky JL, Kearney L;  
 XX  
 DR WPI; 2002-463570/49.  
 DR P-PSDB; ABG61549.  
 XX  
 PT New transporters and ion channels (TRICH) polypeptides, useful for  
 PT diagnosing, preventing, and treating disorders associated with an  
 PT abnormal expression or activity of TRICH, e.g. immunological, muscular or  
 PT renal disorders.  
 XX  
 PS Claim 5; Page 176-177; 178pp; English.  
 XX  
 CC The invention relates to human transporters and ion channels (TRICH)  
 CC polypeptides, a naturally occurring amino acid sequence 90 % identical to  
 CC TRICH, a biologically active fragment of TRICH or an immunogenic fragment  
 CC of TRICH. Also included are an isolated polynucleotide encoding TRICH, a  
 CC recombinant polynucleotide comprising a promoter sequence operably linked  
 CC to the TRICH polynucleotide, a cell transformed with the recombinant  
 CC polynucleotide, a transgenic organism comprising the recombinant  
 CC polynucleotide, an isolated antibody that binds specifically to TRICH,  
 CC and screening for compounds which bind to TRICH, modulate TRICH, modulate  
 CC TRICH expression or are antagonists of TRICH. The polypeptides are  
 CC useful for diagnosing, treating, and preventing transport, neurological,  
 CC muscle, immunological disorders (e.g. scleroderma, systemic lupus  
 CC erythematosus, allergies), cell proliferative disorders such as cancers  
 CC (e.g. leukaemia, cervical or breast cancers), neurodegenerative disorders

(e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes, Grave's disease), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Good pasture's syndrome), viral, bacterial, fungal, parasitic, protozoal and helminthic infections, cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis) and many other diseases and disorders detailed in the specification. They can also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels. TRICH or its fragments may also be used in screening for compounds that specifically bind to and modulate the activity of TRICH. The polynucleotides can be used to create knock-in humanised animals or transgenic animals to model human disease. The present sequence encodes a TRICH protein

SQ Sequence 2235 BP; 395 A; 657 C; 715 G; 468 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.61e-216 Length: 2235  
 Score: 2076.50 Matches: 406  
 Percent Similarity: 97.83% Conservative: 0  
 Best Local Similarity: 97.83% Mismatches: 1  
 Query Match: 93.75% Indels: 9  
 DB: 6 Gaps: 2

US-10-016-647-2 (1-425) x ABK83228 (1-2235)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20  
 DB 428 ATGACCTTCGGGCGCAGCGGGCGGCTTCGGTGTCTGCTACGTGGCGGCGCCGGTAT 487  
 QY 21 SerIleuSerArgGluLeuLeuLysAspPheProIleuArgArgValSerArgLeuHisGly 40  
 DB 488 TCCTGTCTCCGGGAGCTGCTGAAGGACTTCCCGCTCCGCGGTGAGCGGTGCACGCG 547  
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
 DB 548 TGGCGGTCCGAGCGCGAGCTGCTCGAGGTGTGGAGCACTACGACCGCGGCGCACGAG 607  
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80  
 DB 608 TACTTCTTCGACCGGCACCTCGAGGCTTCGGGCTTCATCTGCTTACGTGGCGGCCAC 667  
 QY 81 GlyValSerArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
 DB 668 GGCAGCTGGCTTCGCGCGCGGAGTGTGGAGCTCTCTTCTACACGAGATGATCTAC 727  
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120  
 DB 728 TGGGGCTCGAGGCGCGCACCTCGAGTACTGCTGCAGCGCGCTCGACGCGCATG 787  
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
 DB 788 TCGACACCTTACACCTTCTACTCGGCGGAGCGCGGCGGTGCTGGCGCGCGACGAGGCG 847  
 QY 141 ArgProGlyGlyAla-GluAlaAlaProSerArgArgTyrLeuGluArgMetArgArgTh 160  
 DB 848 CGCCCC--GGCGCGGAGCGGCTCCCTCCAGGCGCTGCTGGAGCGCATCGCGCGGAC 904  
 QY 160 rPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180  
 DB 905 CTTTCGAGGAGCGCCACATC-----CTGGTAGCGGTGCTGGTGGTGT 945  
 QY 180 eValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAl 200  
 DB 946 CGTGATCGTGTCCATGTTGCTGCTGCGCCAGCAGCTTGCCTGCGGCGCACGCGAGC 1005  
 QY 200 alaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTr 220  
 DB 1006 CGCCGACAAACCGCAGCTGGATGACGGAGCAGGATAATTGAAGCTATCTGATAGGTG 1065  
 QY 220 pPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheVally 240

Db 1066 GTTCACTCGCGAGTCATCGTCGAGGTTTCATTGCTCTCCAAACACAGTGTGAGTTGTCAA 1125  
 QY 240 sArgProLeuAenillelleAspLeuLeuAlaileThrProTyrrilleSerValLeuMe 260  
 Db 1126 GAGACCCCTGACATCAITGATTTTACTGGCATATCAGCGGCTATTACATCTCTGTGTTGAT 1185  
 QY 260 tThrValPheThrGlyGluAenSerGlnLeuGlnArgAlaGlyValThrLeuArgValLe 280  
 Db 1186 GACAGTGTTTACAGCGGAGACTCTCACTCCAGAGGGCTGAGTCACCTTGAGGGTACT 1245  
 QY 280 uArgMetMetArgillePheThrValilleYsLeuAlaArgHisPheilleGlyLeuGlnth 300  
 Db 1246 TAGAATGATGAGCAATTTTGGGTGATTAAGCTTCCCGCTCACTTCATTTGCTTTCAGAC 1305  
 QY 300 rIeuGlyLeuThrLeuYsArgCysTyrrArgGluMetValMetLeuLeuValPheilleCy 320  
 Db 1306 ACTCGGTGTGACTCTCAACAGTGTCTACCGAGAGATGTTATGTTACTTGTCTTCATTG 1365  
 QY 320 sValAlaMetAlailePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuG 340  
 Db 1366 TGTTCCTCATGGCAATCTTTAGTGCATTTCTCAGCTTCTTGAAACATGGCTGGACCTGGA 1425  
 QY 340 uThrSerAsnYsAspPheThrSerilleProAlaAlaCysTrpThrValillelleSerMe 360  
 Db 1426 AACATCCCAACAGGACTTTACCGACATTCCTGCTGCTGCTGGTGGGTGATTTATCTCAT 1485  
 QY 360 tThrThrValGlyTyrrGlyAspMetTyrrProilleThrValProGlyArgilleLeuGly 380  
 Db 1486 GACTACAGTGGCTATGAGATATGATCTATCATGCTGCTGGAAGAATCTTGGAGG 1545  
 QY 380 yValCysValValSerGlyilleValleuLeuAlaLeuProilleThrPheilleTyrrHis 400  
 Db 1546 AGTTTGTGTGTGACAGTGAATTTGTTATTTGTCATTACCTATCATCTTTTATCTACCAT 1605  
 QY 400 rPheValGlnCysTyrrHisGluLeuYsPheArgSerAlaArg 414  
 Db 1606 CTTTGTGACGTTTATCATGAGCTCAAGTTAGATTCGTAGG 1648  
 RESULT 9  
 AAD33662  
 ID AAD33662 standard; cDNA; 2312 BP.  
 XX  
 AC AAD33662;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Human TRICH-17 cDNA.  
 XX  
 KW Human; transporter and ion channel; TRICH-17; transport disorder; angina;  
 KW amyotrophic lateral sclerosis; cystic fibrosis; neurodegeneration; angina;  
 KW cardiac disorder; polymyositis; diabetes; neurodegeneration; cancer;  
 KW depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;  
 KW cell proliferated disorder; infertility; arteriosclerosis; gene therapy;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;  
 KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;  
 KW acquired immune deficiency syndrome; immunological disorder; scleroderma;  
 KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;  
 KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;  
 KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;  
 KW muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;  
 KW gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT 325..1845  
 FT /\*tag= a  
 FT /product= "Human TRICH-17 protein"  
 XX  
 PN WC0200212340-A2.  
 XX  
 PD 14-FEB-2002.  
 XX

PF 01-AUG-2001; 2001WO-US024217.  
 XX 03-AUG-2000; 2000US-0223269P.  
 PR 10-AUG-2000; 2000US-0224456P.  
 PR 18-AUG-2000; 2000US-0226410P.  
 PR 25-AUG-2000; 2000US-0228140P.  
 PR 31-AUG-2000; 2000US-0230067P.  
 PR 08-SEP-2000; 2000US-0231434P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 FA Yue H, Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn MR;  
 XX Yang J, Yao MG, Lal P, Wallia NK, Gandhi AR, Hafalia AJA, Nguyen DB;  
 PI Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;  
 PI Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;  
 PI Sanjanwala SS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;  
 PI Das D, Kallikis D, Khan FA, Seilhamer JJ;  
 XX WPI; 2002-206330/26.  
 DR P-PSDB; AAE21173.  
 DR  
 PT New human transporters and ion channels polypeptides and polynucleotides  
 PT for diagnosing, preventing or treating transport, neurological, muscle,  
 PT immunological and cell proliferative disorders.  
 XX  
 PS Claim 91; Page 217; 230pp; English.  
 XX  
 CC The invention relates to human transporter and ion channel polypeptides  
 CC designated TRICH and nucleic acid molecules encoding such polypeptides.  
 CC TRICH sequences are useful for diagnosis, treatment and prevention of  
 CC transport, muscle, neurological, immunological and cell proliferative  
 CC disorders. Transport disorders include akinesia, amyotrophic lateral  
 CC sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular  
 CC dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,  
 CC myocarditis, prostate cancer, cardiac disorders associated with transport  
 CC e.g. polymyositis, bradyarrhythmia, dermatomyositis, angina, neurological  
 CC disorders associated with transport e.g. amnesia, bipolar disorder,  
 CC depression, Tourette's disorder, schizophrenia, other disorders  
 CC associated with transport e.g. neurofibromatosis, sickle cell anaemia,  
 CC Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,  
 CC goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell  
 CC proliferated disorders include cancer, actinic keratosis, cirrhosis,  
 CC arteriosclerosis, atherosclerosis, bursitis, hepatitis and Parkinson's  
 CC Neurological disorders include Alzheimer's, Pick's and Parkinson's  
 CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's  
 CC disease, multiple sclerosis, dementia and other extrapyramidal disorder,  
 CC motor neuron disorder, prion disease, metabolic disease of the nervous  
 CC system and other developmental disorders of the central nervous system,  
 CC neuromuscular disorders, metabolic, endocrine and toxic myopathies,  
 CC periodic paralysis, mental disorders including mood anxiety; and  
 CC immunological disorders include acquired immune deficiency syndrome  
 CC (AIDS), adult respiratory distress syndrome, Addison's disease,  
 CC allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,  
 CC Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,  
 CC haemodialysis, uveitis, viral, bacterial, fungal, parasitic, protozoal,  
 CC hematitic infections and trauma, and muscle disorders include cardiac  
 CC myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The  
 CC TRICH polynucleotides are used in gene therapy. The present sequence is  
 CC human TRICH-17 cDNA  
 XX  
 SQ Sequence 2312 BP; 475 A; 607 C; 674 G; 556 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 4,43e-181 Length: 2312  
 Score: 1758.00 Matches: 351  
 Percent Similarity: 83.37% Conservative: 0  
 Best Local Similarity: 83.37% Mismatches: 0  
 Query Match: 79.37% Indels: 70  
 DB: 6 Gaps: 1  
 US-10-016-647-2 (1-425) x AAD33662 (1-2312)

Qy 5 ArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArg 24  
 Db 790 CGCAGCGGGCGCGCTCGGTGCTGTAACGCTGGGGCGCGCGCTGATTCGCTGTCGCGG 849  
 Qy 25 GluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGlyCysArgSerGlu 44  
 Db 850 GACCTGCTGAAGACCTTCGCGCTGCGCGCTGAGCGCGCTGCACGGCTGCGCTCCGAG 909  
 Qy 45 ArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGluTyrPhePheAsp 64  
 Db 910 CGCGAGCTGCTCGAGGTGCGAGCGACTACGACCGCGAGCGCAACGAGTACTTCTTCGAC 969  
 Qy 65 ArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArg 84  
 Db 970 CGGACCTCGGAGCGCTTCGCGCTTCATCTGCTCTAC----- 1005  
 Qy 85 PheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGlu 104  
 Db 1005 ----- 1005  
 Qy 105 GlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMetSerAspThrTyr 124  
 Db 1005 ----- 1005  
 Qy 125 ThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGlyGly 144  
 Db 1005 ----- 1005  
 Qy 145 AlaGluAlaProSerArgArgTyrTrpLeuGluArgMetArgThrPheGluGluPro 164  
 Db 1006 -----CGCGCTCCCTCCAGCGCTGCTGCGAGCGCATCGCGGACCTTCGAGGAGCC 1059  
 Qy 165 ThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPheValIleValSer 184  
 Db 1060 ACCTGCTGCTGCGCGCGAGATCCCGCTAGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTG 1119  
 Qy 185 MetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAlaAlaAspAsnArg 204  
 Db 1120 ATGGTGGTGTGCGCGAGCAGCTTGGCGAGCTGCGCAACGCGAGCGCGCGCAACCGC 1179  
 Qy 205 SerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224  
 Db 1180 AGCCTGATGACCGGAGCAGGATTAATGAAGCTATCTGCATAGGTGGTTCATCGCCGAG 1239  
 Qy 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244  
 Db 1240 TGCATCGTGAGGTTCATTGTCTCAAAACAAAGTGTGAGTTCGCAAGAGACCCCTGAAC 1299  
 Qy 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264  
 Db 1300 ATCATTGATTACTGGCAATCACCGCGTATTACATCTCTGTGTGATGACAGTGTTTACA 1359  
 Qy 265 GlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArg 284  
 Db 1360 GCGGAGAACTCTCACTCCAGAGGCTGGAGTCACCTTGAGGGTACTAGATGATGAGG 1419  
 Qy 285 IlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThr 304  
 Db 1420 ATTTTGTGGTGATTAAAGCTTGCCGCTCATCTTCATTGGTCTTCAGACACTCGGTTTGACT 1479  
 Qy 305 LeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaAlaMetAla 324  
 Db 1480 CTCAAACGTTGCTACCGAGAGATGGTATGTTACTTGTCTTATTTGTTGTCATGCGCA 1539  
 Qy 325 IlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLys 344  
 Db 1540 ATCTTTAGTGCACTTCTCAGCTTCTGAACATGGCTGGAGCTGGAAACATCCAAACAG 1599  
 Qy 345 AspPheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGly 364  
 Db 1600 GACTTTACACAGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659

Qy 365 TyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGlyValCysValVal 384  
 Db 1660 TATGGAGATATGATATCTATCAGAGTCCCTGGAGAAATTTTGGAGAGTTTGTGTGTC 1719  
 Qy 385 SerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCys 404  
 Db 1720 AGTGAATTTGTTCTTATGGCATTACCTATCATTATCTACCATAGCTTTGTGCAGTGT 1779  
 Qy 405 TyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeu 424  
 Db 1780 TATCATGAGCTCAAGTTTATGCTCTAGTATAGTAGGAGCCTCTCCACTGAATTCCTG 1839  
 Qy 425 Asn 425  
 Db 1840 AAT 1842  
 RESULT 10  
 ADD01469  
 ID ADD01469 standard; cDNA; 950 BP.  
 XX  
 AC ADD01469;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Mouse TCH136 cDNA sequence fragment.  
 XX  
 KW ds; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;  
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;  
 KW cytoskeletal; antiaesthetic; antiarthritic; cerebroprotective;  
 KW antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;  
 KW glucose transporter; potassium ion channel protein; diabetes;  
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;  
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;  
 KW sepsis; gastric hypertrophy; reproductive disorder; pneumonia;  
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;  
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;  
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;  
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;  
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.  
 XX  
 OS Mus sp.  
 XX  
 FN WO2003054190-A1.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 19-DEC-2002; 2002WO-JP013290.  
 XX  
 PR 21-DEC-2001; 2001JP-00389361.  
 PR 25-DEC-2001; 2001JP-00392577.  
 PR 26-DEC-2001; 2001JP-00394947.  
 PR 26-DEC-2001; 2001JP-00395467.  
 PR 06-FEB-2002; 2002JP-00030010.  
 PR 08-FEB-2002; 2002JP-0003095.  
 PR 06-JUN-2002; 2002JP-00165336.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Nakanishi A, Sagiya Y, Uno Y;  
 XX WPI; 2003-541817/51.  
 XX  
 DR Glucose transporter TCH099, vesicular glutamate transporter TCH177 and  
 PT potassium channel protein TCH136 and DNA encoding them for diagnosis,  
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and  
 PT digestive disorders.  
 XX  
 PS Example 21; SEQ ID NO 105; 221pp; Japanese.  
 XX  
 CC The invention relates to a novel glucose transporter TCH099, vesicular  
 CC glutamate transporter TCH177 and voltage-dependent potassium ion channel  
 CC protein TCH136. The sequences are useful in the treatment, prevention and









CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1401 BP; 151 A; 515 C; 515 G; 220 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 11e-85 Length: 1401  
 Score: 880.50 Matches: 182  
 Percent Similarity: 62.24% Conservative: 85  
 Best Local Similarity: 42.42% Mismatches: 125  
 Query Match: 39.75% Indels: 37  
 DB: 5 Gaps: 8

US-10-016-647-2 (1-425) x AAS75631 (1-1401)

Qy 4 GlyArgSerGlyAlaAlaSerValValLeuAenValGlyGlyAlaArgTyrSerLeuSer 23  
 Db 34 GGGGAGCCCGCCCGCCGACATCATCAGTGGGGGCTGCGCGTGGCGCTGGCA 93  
 Qy 24 ArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGlyCysArgSer 43  
 Db 94 TGGGCGCGCTGGCGGATGCGCCCTCGCGCGCTGCGCGCTGCGCGCTGCGCGCGC 153  
 Qy 44 GluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGluTyrPhePhe 63  
 Db 154 CACGACGACTGCTGGCGCTGTGTGACGACTGACGAGTGGCGGCGAGTCTCTTC 213  
 Qy 64 AspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHisGlyLysLeu 83  
 Db 214 GACCGCAGCCGCGCGCTTCCGCGCATGCTGGCGCTTTTGGCGCA---GGGAAGCTG 270  
 Qy 84 ArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeu 103  
 Db 271 CGACTCTCGGGGCGCGCTGGCGCTGCGCTTCCGCGACGAGCTGCGCTACTTGGGGCATC 330  
 Qy 104 GluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAspArgMetSerAspThr 123  
 Db 331 GACGAGCGCGCTGGAGCGCTGCTGCTGCGCGCTGCGCGCTGCGCGCGAGGAGCGC 390  
 Qy 124 TyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArgProgly 143  
 Db 391 -----GCGAGGCG 408  
 Qy 144 -----GlyAlaGluAlaAlaProSerArg----- 151  
 Db 409 CCGACGAGCG 468  
 Qy 152 ---ArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAla 170  
 Db 469 CAGCG 528  
 Qy 171 GlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeuCysAla 190  
 Db 529 AGCTCTTCGCTGCGTGGCGCTGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 588  
 Qy 191 SerThrLeuProAspTrpArgAlaAlaAlaAlaAspAsnArgSerLeuAspArgSer 210  
 Db 589 AGCACCATGCGGACATCCGC---GCCGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCG 645  
 Qy 211 Arg-----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVal 227  
 Db 646 CGCAGCCTGTCTGCTGGAGACCGGTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705

Qy 228 ArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleLeuAsp 247  
 Db 706 CGCTCCCTCGAGCGGAGGAGGAGTGGCTTCTGCGCGCGCGCCACATCATTTGAC 765  
 Qy 248 LeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsn 267  
 Db 766 ATCTGGGCTCTCTGCGCTTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 825  
 Qy 268 SerGln-----LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle 285  
 Db 826 GGGACCAAGCTCTCGGAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885  
 Qy 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeu 305  
 Db 886 CTCTACGCTGATGCGCTGGCGGCGCATCTGCTGGGCTGGCTGGCTGGCTGGCTGGCTG 945  
 Qy 306 LysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIle 325  
 Db 946 CGCGCTGCGCGCGCGAGTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1005  
 Qy 326 PheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345  
 Db 1006 TTCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056  
 Qy 346 PheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyr 365  
 Db 1057 TTTCCAGCGTGGCGCGAGTATTGTTGGCGCTCATCTCCATGACACCGCTGGGCTAC 1116  
 Qy 366 GlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSer 385  
 Db 1117 GCGCAGATGTTCCCGCGCGAGCTCCCGGAGGAGTGTGGCGCTCAGCAGCATCTCAGC 1176  
 Qy 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405  
 Db 1177 GGCATCTGCTCATGGCTTCCCGGTCCACCTCCATCTCCACACCTTTTGGCGCTCCTAC 1236  
 Qy 406 HisGluLeuLysPheArgSerAlaArg 414  
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RESULT 13  
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 ID AB224710 standard; DNA; 1560 BP.  
 XX  
 AC AB224710;  
 DT 07-APR-2003 (first entry)  
 XX Human potassium channel subunit Kv6.3 coding sequence.  
 DE  
 KW Potassium channel; Kv6.3; human; anticonvulsant; antiarrhythmic;  
 KW tranquilizer; cytostatic; virucide; neurotropic; neuroprotective;  
 KW epilepsy; long QT syndrome; muscular ataxia; arrhythmia; gene therapy;  
 KW chromosome 16q24.1; gene; ds.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1560  
 FT /\*tag= a  
 FT /note= "Human Kv6.3"  
 XX  
 FN WO200296944-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 31-MAY-2002; 2002WO-EP006082.  
 XX  
 PR 31-MAY-2001; 2001EP-00202060.  
 XX  
 PA (VLAA-) VLAA- INTERUNIVERSITAIR INST BIOTECHNOG.  
 XX  
 PI Snyders DJ, Otttschytch N, Raes A, Van Hoorick D;

XX	WPI; 2003-140443/13.
DR	P-FSDB; ABF58351.
DR	3
XX	
PT	Novel voltage-gated heterotetrameric potassium channel useful for
PT	diagnosing, preventing and/or treating excitability disorders, comprises
PT	Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.
XX	
XX	Disclosure; Page 45-48; 93pp; English.
PS	

Alignment Scores:		4.01e-85	Length:	1560
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QY	31	ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgaspValLeuGluVal	50	
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QY	51	CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe	70	
DB	301	TCCGATGATTACGACAGCAGCAGCAGGAGTTCCTTCGACAGGAGCCCCAGCGGCTTC	360	
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QY	111	CysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp	130	
DB	478	TGCTCCCTGCGGAGCTCTCAGGAAGCTGGAGGAGGCTGGAGGAGCTGGCCAAAGCTGCAC	537	

Qy	131	GlupProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGluAlaAala	149
Db	538	AGGAGAGACGTACTGAGGCACGAGAGGAGACCGCGCGCCC-----GCCTCG	585
Qy	149	ProSerArgArgTrrp-----LeuGluArgMetArgArgThrPheGluGluProThr	165
Db	586	CACCTCTCGCGCTGGGGCTGTGCATGAACCGCTGCGCGAGATGGTGGAAAAACCCGAC	645
Qy	166	SerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPheValIleValSerMet	185
Db	646	TCGGGGTCCCGGGAAGAGTCTTCGTCTGCTCTCCATCTCTTCGTGGCCACACAGCC	705
Qy	186	ValValLeuCysAlaSerThrLeuProAspTrrpArgAsnAlaAlaAlaAspAsnArgSer	205
Db	706	GTACGCTGTGTGTACACACACTCCCGCACTCAGG-----GCAGAGGAGGACCAAGGC	759
Qy	206	LeuAspAspArgSer-----ArgIleIleGluAlaIleCysIleGlyTrrpPhe	221
Db	760	GAATGTCTTCGGAAGTGTACTATATTTTCATCGTGAGACCATCTCGCTGGCTGTCTTC	813
Qy	222	ThrAlaGluCysIleValAlaArgPheIleValSerIysAsnIysCysGluPheValIysArg	241
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Qy	242	ProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTrrpIleSerValLeuMetThr	261
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Qy	262	ValPheThrGlyGlu-----AsnSerGlnLeuGlnArgAlaGly	274
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Qy	295	PheIleGlyLeuGlnThrLeuGlyLeuThrLeuIysArgCysTyrArgGluMetValMet	314
Db	1060	TCGCTGGGGTGCAGACGCTGGGGCTCACCGTGGCGCGTGTGCACAGCTGAGTTCGGCCTG	1119
Qy	315	LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaIleuSerGlnLeuLeu---	333
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Qy	334	---GluHisGlyLeuAspLeuGluThrSerAsnIysAspPheThrSerIleProAlaAala	352
Db	1180	AAGAGTTCGGCGGGTGTGGAG-----TTCACGACATCCCGCGCTCC	1224
Qy	353	CysTrrpTrrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThr	372
Db	1225	TATTGTGGGCCATCATCTCCATGACAACGGTGGGCTACGGGACATGGTGGCCCCGAGT	1284
Qy	373	ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeu	392
Db	1285	GTCCAGGCGAGATGGTGGCCCTACGAGCATCTCTAGCGGGATCTCTCATCATGGCCTTC	1344
Qy	393	ProIleThrPheIleTrrpHisSerPheValGlnCysTrrpHisGluLeuLys	409
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XX	AC		
XX	DT	04-APR-2000 (first entry)	
XX	DE	Human Voltage-gated Potassium channel monomer, Kv6.2 gene.	
XX	KW	Voltage gated potassium channel; Kv6.2; human; excitability; ion flux;	
XX	KW	resting potential; alpha subunit; modulator; hearing/vision problem;	
XX	KW	migraine; central nervous system; CNS; seizure; neuroprotective agent;	



## RESULT 15

AAZ49454  
ID AAZ49454 standard; DNA; 1518 BP.

XX AC AAZ49454;

XX DT 04-APR-2000 (first entry)

XX DE Mouse Voltage-gated Potassium channel monomer, Kv6.2 gene.

XX KW Voltage gated potassium channel; Kv6.2; mouse; excitability; ion flux;  
resting potential; alpha subunit; modulator; hearing/vision problem;  
migraine; central nervous system; CNS; seizure; neuroprotective agent;  
psychotic disorder; reporter; treatment; detection; antibody; probe;  
primer; ds.

XX OS Mus sp.

XX FH Location/Qualifiers

XX mat\_peptide

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XX /label= Mouse\_Kv6.2\_polypeptide

XX /note= "Voltage gated potassium channel subunit"

XX 1381. .1389

XX /<tag= b

XX /note= "This region encodes the amino acid sequence ELK,  
which is represented in the specification as the  
typographical error Kv6.2 (an insertion of the protein  
name)"

XX WO200001811-A1.

XX 13-JAN-2000.

XX 30-JUN-1999; 99WO-US014945.

XX 01-JUL-1998; 98US-0091466P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2000-126937/11.

XX P-PSDB; AAY44564.

XX New voltage-gated potassium channel alpha subunit, useful for identifying  
modulators of voltage-gated channel activity useful for treating central  
nervous system disorders e.g. migraines and as neuroprotective agents.

XX Claim' 5; Page 65-66; 80pp; English.

XX The present sequence is the gene encoding the mouse Kv6.2 monomer, which  
is an alpha subunit of heteromeric voltage-gated potassium channel. It is  
isolated from brain tissue and maintains the resting potential and  
controls the excitability of a cell. Kv6.2 polypeptide can be used to  
CC identify compounds that modulate the ion flux through heteromeric  
voltage-gated potassium channels. Such modulators are used as  
neuroprotective agents and for treating CNS disorders, such as migraines,  
hearing and vision problems, psychotic disorders and seizures. It can  
also be used as reporter molecules in assays and to produce antibodies.  
Kv6.2 DNA sequence can be used to produce specific primers or probes for  
detection purposes

XX Sequence 1518 BP; 271 A; 467 C; 470 G; 310 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 5.38e-84 Length: 1518  
Score: 865.50 Matches: 179  
Percent Similarity: 62.71% Conservative: 85  
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Query Match: 39.07% Indels: 39  
DB: 3 Gaps: 9

US-10-016-647-2 (1-425) x AAZ49454 (1-1518)

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QY 31 ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50  
DB 238 CCGCTGAGCCGCTGAGCAGGCTCCGCTGTGGCGAGCATGAGGAGATCACGAGCTC 297

QY 51 CysAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70  
DB 298 TGCATGACTACGATGAGCAGCAGGAGTCTTCTTCACAGGAAACCCAGCGCTTC 357

QY 71 GlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90  
DB 358 GGGGTGATCTGAGCTTCCTGGCCGCG--GGAAGCTGGTCTCTGCGAGAGATGTC 414

QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110  
DB 415 CCGCTGTCCTTCGGGAGGAGCTGAGCTACTGCGGCATCGAGGAAACCAACCTGGAGCGC 474

QY 111 CysCysGlnArgArgLeuAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130  
DB 475 TGCTGCTGCGCAAGCTGCTGAAGAAGCTG-----GAG 507

QY 131 GluProGlyValLeuGlyArgAspGluAla-----ArgProGlyGly 144  
DB 508 GAGCGCGCAGCTGCGCGGAGGAGCTGCCAGCGCCAGCAGCAGCGCCAGCGCTGC 567

QY 145 AlaGluAlaAlaProSerArgArgTrp-----LeuGluArgMetArgArgThrPhe 161  
DB 568 CACTCCGAGGTGCAGGCTTCACGATGGCGCCGAGCATGAACAGCTGCTGAAATCGTG 627

QY 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValAlaPheVal 181  
DB 628 GAGGACCCACAGTCGGGCTGCCCGGAGGAGTCTTCGCTGCTCCTCGGCTCTTCGTG 687

QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 201  
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QY 202 AspAsnArgSerLeuAspArgSer-----ArgIleIleGluAlaIleCys 217  
DB 742 GAGGCGAGGAGAGATGCATGAGAGTGTATTACATCTTCGTGGTGGATCCATCTGT 801

QY 218 IleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGlu 237  
DB 802 GTGGCTGGTTCGCTGGAGTTTGTGCTGGCTTTGTCCAGCGCCCGCAAAATGTCAG 861

QY 238 PheValLysArgProLeuAsnIleLeuAspLeuAlaIleThrProTyrTyrIleSer 257  
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QY 389 LeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu 408
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QY 409 Lys 409
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GenCore version 5.1.6  
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Title: US-10-016-647-2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; APPLICANT: Jegla, Timothy James  
; APPLICANT: ICAGEN Incorporated  
; TITLE OF INVENTION: Kv6.2, a Voltage-Gated Potassium Channel Subunit  
; FILE REFERENCE: 018512-001410US  
; CURRENT APPLICATION NUMBER: US/09/719,919A  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/091,466  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: WO PCT/US99/14945  
; PRIOR FILING DATE: 1999-06-30  
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; OTHER INFORMATION: human alpha subunit of heteromeric voltage-gated  
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US-09-719-919A-18

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Qy 271 GlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTTPValLys 290  
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Qy 331 GlnLeuLeuGluHis-----GlyLeuAspLeuGluThrSerAsnLysAspPheThrSer 348  
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Db 1267 GTCCCTCGCGAGCTCCCGGAGAGTGTGCTGCTGAGCAGCATCTTTAGCGGATCCTT 1326  
Qy 389 LeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu 408  
Db 1327 ATCATGGCTTCCAGCCACATCCATCTTCACAGCTCTCTACTCTCTACTCTGAGCTG 1386  
Qy 409 Lys 409  
Db 1387 AAG 1389

## RESULT 3

US-08-464-340A-1

; Sequence 1, Application US/08464340A

; Patent No. 5710019

; GENERAL INFORMATION:

; APPLICANT: Li, ET AL.

; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,340A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08449  
FILING DATE: 28 JUL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-415  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2127 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: cDNA  
US-08-464-340A-1  
Alignment Scores:  
Pred. No.: 1,12e-96 Length: 2127  
Score: 855.50 Matches: 178  
Percent Similarity: 60.94% Conservative: 81  
Best Local Similarity: 41.88% Mismatches: 141  
Query Match: 38.62% Indels: 25  
DB: 1 Gaps: 8  
US-10-016-647-2 (1-425) x US-08-464-340A-1 (1-2127)  
Qy 11 ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe 30  
Db 474 ATCATCATCAACGTAGCGCGCATCAAGTACTCGCTCGCTGGACCACTGCTGCGAGTTTC 533  
Qy 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50  
Db 534 CCCTGACGCGCTGGCGCGAGCTCAAGGCTGACCAACTTCGACGACATCTCTCAAGTG 593  
Qy 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70  
Db 594 TGGCATGACTACGACGCTCACCTGCAACAGAGTTCTTCTCGACCGCAACCGCGGGGCTTC 653  
Qy 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90  
Db 654 GGCACTATCTGCTACCTCTCTGCGCGGCGG---GGCAAGCTGCGGCTGCTGCGGAGATGTGC 710  
Qy 91 GluLeuSerPheTyrAsnGluMetIleTyrTTPGlyLeuGluGlyAlaHisLeuGluTyr 110  
Db 711 GCGCTGTCTTCAGGAGGAGTGTCTGTACTGGGCGATCGCGGAGGACCACTTGGACGCG 770  
Qy 111 CysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130  
Db 771 TGTTCAGCGCGCTTACCTCGCAGAAAGATTGAGAGTTCGCGGAGATGTGTGGAGCGGAG 830  
Qy 131 GluProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGlu 146

831 GAAGAGACGACGGCGCTGGACACGAGAGGGCGCGACAGCAGGAGGCCCGCGGAGGGCGAG 890

147 AlaAlaProSerArgArgTgtTLeuGluArgMetArgThrPheGluGluProThrSer 166

891 GGGCGCTCTGGG---CGCTGATCGCGCGACTGCGCAGACATGTTGGAGAGCGCGACTCG 947

167 SerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetVal 186

948 GGGCTGCTGCGCAAGAGTTCGCGCTCGCTCGGTGCTCTTCGTGACCGTCACCGCGCTC 1007

187 ValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAlaAlaAspAsnArg----- 204

1008 AACCTCTCCGTGACACCTTGCCAGCGCTGAGGAGGAGGAGGAGGAGGCCACTGTTCC 1067

205 SerLeuAspAspArgSerArgIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224

1068 CAGATGTGCCACACACGCTTCATCGTGGAGTCGGGTGCGGTGGGCTGGTTCTCCCTGGAG 1127

225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244

1128 TTCTCTCTGGGCTCATTGAGGCGCCACAGATTCGCTTCTTCGGAGCCCGCTGACG 1187

245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThr---ValPhe 263

1188 CTGATCAGACTGGTGGCACTCTGCCCTACTATCATCAGCTGTGTTGGAGAGCGCGCGCC 1247

264 ThrGlyGlu-----AsnSerGlnLeuGlnArgAlaGlyValThrLeu 277

1248 GCAGGCGCTGCAAGCCGGGGGGAACAGTACTGTGACAGAGTGGGGCTGTGTGCTG 1307

278 ArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGly 297

1308 CGGCTGCTCGGGCGCTGCGCATCTGTACGTGATGCGCCTGCGCGCCACTCCCTGGGG 1367

298 LeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuVal 317

1368 CTGCAGACGTGGGGCTCAGCGCGCGCTGCACCGCGAGTTCGGGCTCTCTGCTGCTC 1427

318 PheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeu 337

1428 TTCTCTGCGTGGCCATCGCCCTCTTCGCGCCCTGTCTACGTCTCAGTCAGAGACGAGATG 1487

338 AspLeuGluThrSerAsnLysAspPheThrSerIleProAlaIaCysTrpTrpValIle 357

1488 -----GCCGACCCCGAGTTCACAGCATCCCTCCCTACTCGTGGGCTGTC 1538

358 IleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIle 377

1539 ATCACCATGACGACGTGGACTATGGCGACATGGTCCCCAGGAGGACCCCGGCGCAGGTA 1598

378 LeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIle 397

1599 GTGCGCCCTGAGCAGCATCTGAGCGGATCTGCTCATGCGCTTCCACAGTCACCTCCATC 1658

398 TyrHisSerPheValGlnCysTyrHisGluLeuLys-----Phe 410

1659 TTCACACACTTCTCCCTCTCTACTCGAGCTCAACAGGAGCAGAGAGGGGTGATGTTTC 1718

411 ArgSerAlaArgTyr 415

1719 CGGAGGGCGCAGTTC 1733

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CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449A
FILING DATE: SUBMITTED HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US94-08449A-1

Alignment Scores:
Pred. No.: 1,128-96 Length: 2127
Score: 855.50 Matches: 178
Percent Similarity: 60.94% Conservative: 81
Best Local Similarity: 41.88% Mismatches: 141
Query Match: 38.62% Indels: 25
DB: 8 Gaps: 8

US-10-016-647-2 (1-425) x PCT-US94-08449A-1 (1-2127)

Qy 11 ValValLeuAsnValGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe 30
Db 474 ATCATTCACAGTAGGCGGCATCAAGTACTCGTGCCTGGACCAACGCTGGACGAGTTC 533
Qy 31 ProLeuAArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
Db 534 CGCGTAGCGCGCTCGGCGCAGCTCAAGCCTGCAACCACTTCAGACACATCTCAACGHTG 593
Qy 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
Db 594 TCGGATGACTACGAGTCACCTGCAACGAGTCTCTTCACCGCAACCGCGGGGCTTC 653
Qy 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
Db 654 GGCACATCTCTGACCTCTCTCGCGCGCG---GGCAAGCTGCGGCTGTCGCGGAGATGTGC 710
Qy 91 GluLeuSerPheTyrAsnGluMetIleTyrTyrGlyLeuGluGlyAlaHisLeuGluTyr 110
Db 711 GCGCTGTCTTCAGGAGAGCTGCTGTACTGGGGCATCGCGGAGGACCACTGGAGCGG 770
Qy 111 CysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
Db 771 TGTGTCAAGCGCGCTACCTCGAGAAGATTGAGGAGTTCGCGGAGATGTGTGGAGCGGGAG 830
Qy 131 GluProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGlu 146
Db 831 GAAGAGGACGACCGCTGGACGAGCGGCGCGACAGCGAGGGCCGCCGAGGGCGGAG 890
Qy 147 AlaAlaProSerArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSer 166
Db 891 GCGCGCTGGGG---CGCTGATCGCGCGACTGCTGCGACATGTGTGAGAGCGCGCACTCG 947

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QY 231 ValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAla 250
Db 1266 TGTGTGGGAGAGGTGTGGCTTCTTAAGAAAGGTGCCAAACATCATAGACCTCTTCC 1325
QY 251 IleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSer----- 268
Db 1326 ATCTTCCCTTCTACATCACTCTTCTGGTAGAGACCTAAGTGGGAGCCAGACGAG 1385
QY 269 GlnLeuGlnArgAlaGlyValThrLeuArgValLeuMetMetArgIlePheTrpVal 288
Db 1386 GAGCTGGAGAACGTGGGGGCGCATTTCCAGGTGTTCAGGCTCTCAGGGCTCTGGCGCAT 1445
QY 289 IleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCys 308
Db 1446 CTAAAGCTGGCGAGACATTTCCACAGGATTACGCTCTCTTGGGATGACAAATCACCCAGTGT 1505
QY 309 TyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAla 328
Db 1506 TACGAAGAGTGGCGCTACTGTCTCTATTCTATCGTGGGAATCTCTATATTTCAACT 1565
QY 329 LeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSer 348
Db 1566 GTAGAAATCTTGTCTGAGCAAGCATTTCTGTGACCAACCC-----TTCAAGT 1613
QY 349 IleProAlaAlaCysTrpTrpValIleIleSerMetThrValGlyTyrGlyAspMet 368
Db 1614 GTCCCTTGTGTGTGGTGGCCACCACCTCTATGACTACTGTGGGATATGGGACATT 1673
QY 369 TyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIleVal 388
Db 1674 AGACCAAGACACCAACAGCAAGCAATCGTGGCTTCATGTGTATATTATCGGGAATCTT 1733
QY 389 LeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu 408
Db 1734 GTCTTGGCTTGGCTTATCTATTATTAACGATCGCTTCTGTGTGCTACTTCACTTG 1793
QY 409 LysPheArgSerAla-----ArgTyrSerArgSerLeu 419
Db 1794 AAACCTCAAGGAAGACGCTGTAGACAGCGTGAAGCGCTTAAGAAAGCTTACCAAGAATATA 1853
QY 420 SerThrGlu 422
Db 1854 GCCACTGAC 1862

```

## RESULT 6

```

US-09-181-339-6
; Sequence 6, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033 30
; CURRENT APPLICATION NUMBER: US/09/181,339
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (449)...(1924)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2494)
; OTHER INFORMATION: n = A,T,C or G

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## US-09-181-339-6

## Alignment Scores:

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Pred. No.: 1,13e-76 Length: 2494
Score: 697.00 Matches: 149
Percent Similarity: 55.63% Conservative: 93
Best Local Similarity: 34.25% Mismatches: 149
Query Match: 31.47% Indels: 44
Gaps: 11

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## US-10-016-647-2 (1-425) x US-09-181-339-6 (1-2494)

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QY 1 MetThrPheGly-----ArgSerGlyAlaAlaSer-----ValValLeuAsn 14
Db 449 ATGGTGTTCGTGAGTTCATCCATCGCCCTGGCAAGATGAGGAACCTGTCACTTGAAC 508
QY 15 ValGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArgArg 34
Db 509 GTGGGGGGCTTTAAGCAGTCTGTGGATCAAAGTACACTCTCGCGTTCCTCCACACCA 568
QY 35 ValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyr 54
Db 569 CTGGGAAGTGTCTTACCTGCCACTCTGAGAGGCCATCTGGAGCTGTGTGATGACTAC 628
QY 55 AspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeu 74
Db 629 AGCGTGGCAGATAAAGAGTACTACTTTGATCGGAACCCCTTCCTGTTCAGATACGTC 688
QY 75 LeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPhe 94
Db 689 AACTTTTATTAC---ACAGGAAGCTGTCATGTCATGATGAGGAACCTGTGTCTCTCTTC 745
QY 95 TyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArg 114
Db 746 TGCCAGGAGATCGAGTACTTGGGCAATCAATGAGCTCTTCATTGACTCTCTGTAGCAGT 805
QY 115 ArgLeu-----AspAspArgMetSerAsp 122
Db 806 CGGTACAGGAGCGCAAGGAGAGAGCCAGCAGCAAGGACTGGGACCCAGAAAGCAACGAT 865
QY 123 ThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArg----- 137
Db 866 GTGAGCAGACTCCCTCTTTGAAGTACGTCCTCTGTTGAGAAGAGAGCTGGAGAAGTTT 925
QY 138 AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMet 157
Db 926 GATGAGCTGAGATTGGTCAGCTCCGA-----AAGAAGATCTGGATCGA----- 970
QY 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer 177
Db 971 -----ATGGAATCCAGCTTACTGCTGTCGCCAAGCTCATTCCTCTCTCTCC 1021
QY 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
Db 1022 TTGACGTGTGTGTGCTTCCATAGTGGCCATGTGTGTGCACAGCATGTGGAATTCAG 1081
QY 198 AsnAlaAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIle--- 216
Db 1082 AAC-----GAGGATGAGAGTGGATGAC-----CCTGTGCTGAAGTGTGGAG 1126
QY 217 -----CysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsn 234
Db 1127 ATTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1186
QY 235 LysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyr 254
Db 1187 CAAAAGAAAGTCTGGAAAAACCTCTGAAACATCATTTGACTTTGTTTCTATCATTCCTCTC 1246
QY 255 TyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGly 274
Db 1247 TATGCCACGTTGGCTGTGGACACCAAGGAAGAGAGTGGAGACATTGAGATATATGGGC 1306
QY 275 ValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHis 294

```

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Db      1307 AAGGTGGTCCAGATCCTTCGGCTCATGAGATTTCCGAATTCAGAGCTTGCCCGGCAC 1366
Qy      295 PheileGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet 314
Db      1367 TCTGTAGGCTTCGGTCTTCCTGGGCCACACTGAGGCACAGTTACCATGAGTGGGGCTA 1426
Qy      315 LeuLeuValPheileCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGlu 334
Db      1427 CTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1474
Qy      335 HisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyr 354
Db      1475 TACTCTGTGGAGAAGATGAACACAGTCCAGTCTCACCAGATCCCATCTGCTGGTGG 1534
Qy      355 TrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValPro 374
Db      1535 TGGGCCACTATCAGTATGACCACTGAGTGGGCTATGGAGACACCCACCCAGTACCTTACCT 1594
Qy      375 GlyArgIleLeuGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIle 394
Db      1595 GGGAAATCATTCGACGACATGTATTAATCTGTGGAAATCTTAGTGTAGCCCTCCCAATT 1654
Qy      395 ThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
Db      1655 ACCATCATCTTCACAAAGTTTCCAAAGTACTACCAAGACAGAAA 1699

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## RESULT 7

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US-09-181-339-11
; Sequence 11, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsaveth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033.30
; CURRENT APPLICATION NUMBER: US/09/181,339
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2266
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (308)...(1783)
US-09-181-339-11

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Alignment Scores:
Pred. No.:      2 658-75      Length:      2266
Score:          685.50      Matches:      157
Percent Similarity: 52.99%      Conservative: 91
Best Local Similarity: 33.55%      Mismatches: 155
Query Match:      30.95%      Indels:      65
DB:                4          Gaps:        14

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US-10-016-647-2 (1-425) x US-09-181-339-11 (1-2266)

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Qy      1 MetThrPheGly-----ArgSerGlyAlaAlaSer-----ValValLeuAsn 14
Db      308 ATGGTGTGTTGGTGGAGTTTTCATCGCCCTGGACAAAGACGAGGAACCTTGTCAACCTGAAT 367
Qy      15 ValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLysAspPheProLeuArgArg 34
Db      368 GTGGGGGGCTTTAAGCAGTCTGTTGACCAAAACACCCCTCTCCGGTTTCTTCACACACAGA 427
Qy      35 ValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAspTyr 54

```

```

Db      428 CTGGGGAGAGCTGCTTACTTCCCATTTCTGAAGAGCCATTTCTGGAGCTGTGTGATGATTAC 487
Qy      55 AspArgGluArgAsnGlnTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeu 74
Db      488 AGTGTGCCCATGAAGAAATACTACTTGTATCGGAATCCCTCTTGTTCAGATATGTTTG 547
Qy      75 LeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPhe 94
Db      548 AATTATTATTAC---ACGGGAAGCTGCATGTCATGGAGAGAGCTGTGCGTATTCTTCATTC 604
Qy      95 TyrAsnGluMetIleTyrTyrGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArg 114
Db      605 TGCAGAGAGATCGAGTACTTGGGCGCATCACAGAGCTCTTTCATTGATCTTCTGCTGAGCAAT 664
Qy      115 ArgLeu-----AspAspArgMetSerAsp 122
Db      665 CGCTTACCAGAAACGCAAGAGGAGAAACCCAGAGAGAGCTGGGACCCAGAAAAGCCATGAT 724
Qy      123 ThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArg----- 137
Db      725 GTGAGTACCCAGCTCCTCGTTTGAAGAGTCGTCTCTGTTTGAGAAAGAGCTGGAGAGATTT 784
Qy      138 AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTyrPheLeuGluArgMet 157
Db      785 GACACACTGCGATTTGGTCTGAGCTCCGG-----AAGAAATCTGGATTAGA----- 829
Qy      158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer 177
Db      830 -----ATGGAGAATCCAGCGTACTGCTCTCGCTAAGCTTATCGTATCTCTCTCC 880
Qy      178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArg 197
Db      881 TTGAGCTGTGTGGCTCCATCGTGGCCATGTGCGTTCACAGCATGTGCGAGTTCCAG 940
Qy      198 AsnAlaAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIle--- 216
Db      941 AAT-----GAGGATGGAGAGTGGATGAT-----CCGTTGCTGGAGAGGTGGAG 985
Qy      217 -----CysIleGlyTyrPheThrAlaGluCysIleValArgPheIleValSerLysAsn 234
Db      986 ATCGCGTGCATTCGCTGTTTACCGGGGAGCTTCCGCTCCGCTGGCTGCGCTCTGT 1045
Qy      235 LysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyr 254
Db      1046 CAAAGAAATTCGGAAAAACCCCTCTGAACATCATTTGCTCTATTATTTCCCTTC 1105
Qy      255 TyrIleSerValLeuMetThrValPheThrGlyLysAsnSerGlnLeuLysArgAlaGly 274
Db      1106 TATGCCACGTTGGCTGTAGACACCAAGGAGAGAGTGGAGATATTGAGAACATGGGC 1165
Qy      275 ValThrLeuArgValLeuArgMetMetArgIlePheTyrPheValIleLysLeuAlaArgHis 294
Db      1166 AAGGTGGTCCAGATCCTTACGGCTTATGAGGATTTTCGAAATTTCTAAAGCTTGCCCGGCAC 1225
Qy      295 PheIleGlyLeuGlnThrLeuGlyLeuThrLysArgCysTyrArgGluMetValMet 314
Db      1226 TCGGTAGGATTTGGTCTCTAGTGGCCACACTGAGACACAGTACCATTGAAGTTGGCTT 1285
Qy      315 LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGlu 334
Db      1286 CTGCTTCTCTCTCTCTGTTGGGCAATTCATTTCTCTGTGCTTATCTACTCTCGTGGAG 1345
Qy      335 HisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyr 354
Db      1346 AAA-----GATGACCACATCCAGC-----CTACACAGCATCCCATCTGCTGGTGG 1393
Qy      355 TrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValPro 374
Db      1394 TGGGCCACCATCAGCATGACATCTGTGGGCTATGGAGACACCCACCCGGTCACTTGGCG 1453
Qy      375 GlyArgIleLeuGlyValCysValSerGlyIleValLeuLeuAlaLeuProIle 394
Db      1454 GGAAGCTCATCGCCAGCACATCATCTGTGGCATCTGTGGTGTGGTGGCTTCCCATC 1513

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; LOCATION: (154)....(1647)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(2799)
; OTHER INFORMATION: n = A,T,C or G
US-09-181-339-2

Alignment Scores:
Pred. No.:      8,02e-72      Length:      2799
Score:          659.00      Matches:      157
Percent Similarity: 51.58%      Conservative: 72
Best Local Similarity: 35.36%      Mismatches: 169
Query Match:      29.75%      Indels:      46
DB:               4          Gaps:      10

US-10-016-647-2 (1-425) x US-09-181-339-2 (1-2799)

QY 13 LeuAsnValGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeu 32
DB 220 GTGACGTGGCGAGTGGCGGCGCTGCTGAGCGCGCGCCCTTCCGCGGC 279
QY 33 ArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuValCysAsp 52
DB 280 ACGCGCTGGCGCGCTACAGCGCGCGGCTGCTCGAGGAGCGCGCGCGCTGTGCGAC 339
QY 53 AspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe--Gly 71
DB 340 GACTACGACGCGCGCGCGGACGAGTCTACTTTGATCGGCATCCGGGCTTCTTTCGCGC 399
QY 72 PheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGlu 91
DB 400 GTCCCTACACTTACCGCACCGGCGAC-----CTGCACGTCTCTAGACGAGCTGTGCGTC 453
QY 92 LeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCys 111
DB 454 TTGCGCTTGGCGAGGCTGACTACTGGGCGCTGGCGGAGACGCGCTGCGCCACGTCG 513
QY 112 CysGlnArgArgLeuAspArgMet-----Ser 121
DB 514 TGCGCGCGCGGATCTGGAGCGCGTGTGGCGGCGCTCGCGCCCTGGGACGAGCACAGC 573
QY 122 AspThrTyrThrPheTyrSer-----AlaAspGluProGlyValLeuGlyArgAspGlu 139
DB 574 GAGCGCGCGAGCGTGGACCGCTGCTCCGACGAGATCTCGACGTGCGAGCGGAGCTG 633
QY 140 AlaArgProGlyGlyAlaGluAlaAlaProSerArgArg-----TrpLeuGluArgMet 157
DB 634 GCGCGCTAATGGTGGCGCTCGCTGGCGCGCTGGCGCGCTGCTCTGCTGCTC----- 684
QY 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer 177
DB 685 -----ACCATGAGAGATCCAGCTACTCGCTGCCAGCAAGCTCTTCAGCTGCGTATCC 738
QY 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
DB 739 ATCGCGGTGTGCTGCTCCCTCCATCGCTGCATGTGCATCCACAGCTGCGCGAGTACCA 798
QY 198 -----AsnAlaAlaAspAsnArgSerLeu----- 206
DB 799 GCTCGGAGCGCGCGCGCGTGGTGGTGGCGCGCTGGCGCGCTGGCGCGCGAGAGGAGTG 858
QY 207 -----AspAspArgSerArgIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224
DB 859 CGGACGACCGGTGTGCGCGCGCTGGAGTACTTCTGATCGCTGGTTCAGTTCGAG 918
QY 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
DB 919 GTGTCGTGCGCTGCTGCTGCTGCCAGCGCAACTTCTTCTGCCACCGCTCAAC 978
QY 245 IleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264
DB 979 CTCATTGACATCGTGTGCTGCTGCTTCTATCTCACACTGCTGCTGGCGCGAGCGCTT 1038

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265 GlyGlu-----AsnSerGlnLeuGlnArgAlaGlyValThrLeuArgVal 279  
1039 GGTACCAGCGCGGAGCGAGCGGGGAGGAGCTCGGGACCTGGGCAAGTAGTGCAGAGTG 1098  
280 LeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGln 299  
1099 TTCGCGCTCATCGCACTTCCGCGTCTCAAGCTGGCGGCCACTCCACGCGGCTCGGT 1158  
300 ThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIle 319  
1159 TCGTGGGCGCGCACGCTCAAGCACAGCTACCGTGAGTGGGCTCTTACTGCTGTACCTG 1218  
320 CysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeu 339  
1219 GCCGTGGTGTGTCAGTGTCTTCGCGGTGGCTTACACGCCGAGAA----- 1266  
340 GluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSer 359  
1267 -----GAAAGCGAGGCTTTCACACAATCCCTGCTGCTGGTGGGCGCACAGTGAGC 1320  
360 MetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGly 379  
1321 ATGACCAAGTGGGCTATGGGATGTGTCGACAGACTGTGGTGGCAAGCTGGCGGCGC 1380  
380 GlyValCysValSerGlyIleValLeuAlaLeuProIleThrPheIleTyrHis 399  
1381 TCGGCTGCATCTCGGGGCGATCTGCTGGTGGCTCCCTCCCATCACCATCTTCAAC 1440  
400 SerPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeu 419  
1441 AAGTTTTCCCACTTCTACCGCGCGCAGAGGACTGGAGCGCGCGCTGGCGAGCAGCGGT 1500  
420 SerThrGluPhe 423  
1501 CAGCGCGAGTTT 1512

RESULT 11  
US-08-464-340A-3  
; Sequence 3, Application US/08464340A  
; Patent No. 5710019  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,340A  
; FILING DATE: June 5,1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: PCT/US94/08449  
; APPLICATION NUMBER:  
; FILING DATE: 28 JUL 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-464-340A-3

Alignment Scores:
Pred. No.: 6, 72e-69 Length: 2483
Score: 635.00 Matches: 150
Percent Similarity: 54.73% Conservative: 87
Best Local Similarity: 34.64% Mismatches: 171
Query Match: 28.67% Indels: 26
DB: 1 Gaps: 9

US-10-016-647-2 (1-425) x US-08-464-340A-3 (1-2483)
QY 5 ArgSerGlyAlaAlaSer-----ValValLeuAenValGlyValAlaArgTyr 20
DB 727 CAGAGTCGCGTGCAGGAGCAGACATAGATAGTGCATCAACGTGGGGGGGTGCGGAG 786
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
DB 787 GTGCTGTAGCGGAGCTCTCAGTCAGTACCTGAGACCGCGGTGGCGGAGCTCATCAAC 846
QY 41 CysArgSer-----GluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58
DB 847 TGCTTGGTGGGGGTACGACACCATCTTCTCCCTGTGCGAGCTACGACCCCGGCAAG 906
QY 59 AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArg 78
DB 907 CCGAGATCTTACTTTGACGAGGACCGGACCGCTTCAAGTGTGC---ATCGAGGTGTAC 963
QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98
DB 964 TATTTTCGGGAGGTCACATGAAGAAGGAGCATCTGCCCATCTGCTTCAAGAACGAGATG 1023
QY 99 IleTyrTrpGlyLeuGluClyAlaHisIleuGluTyrCysGlyArgArgAspAsp 118
DB 1024 GACTTCTGAGAGGTGACCTCAAGTCTCTGGACGACTGTGTCAAGAGCCACCTGAGCGAG 1083
QY 119 ArgMetSerAspThrTyrThrPheTyrSer-----AlaAspGluProGlyValLeuGly 136
DB 1084 AAGCGGAGGAGCTGGAGGAGATCGC-GGCGCGCTGGCGACTCATCTGGACGACCTGGG 1142
QY 137 ArgAspGluAlaArgProGlyAlaGluAlaAlaProSerArgArg-TrpLeuGluArg 156
DB 1143 CGTGGACGCGGCGCA---GGCGCGCTGGCGCGCTGCCAGAAAGTGGCTGCG- 1191
QY 156 gMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerVa 176
DB 1192 -----AAGTCTCGGAGAACCGGAGTCGTCGCGCGCGGGTGGTGGCGAGCT 1244
QY 176 lSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyr 196
DB 1245 CTCCTTCCTGCTCATCTCGTCTCGTCCGTCGTGTCATGTGTCATGACACCATCCCGAACT 1304
QY 196 pArgAsnAlaAlaAlaAsp--AsnArgSerLeuAspAspArgSerArgIleIleGluAl 215
DB 1305 GCAGTGTGCGAGCGCGGAGGAGCGCGCTGGAGACCGGAGTGGAGAACGTGGAGAC 1364
QY 215 alleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnly 235
DB 1365 GGCGTGCANTGGTGTTCACCTCGGAGTACCTGTCGCGCTCTTCTGTCACCAACAA 1424
QY 235 sCysGluPheValLysArgProLeuAsnIleLeuAspLeuLeuAlaIleThrProTyrTy 255
DB 1425 GCTGCATCTCGCGCTCTCTTCAACATTTGGACGTGTGGCATCTCTCCCTCTTA 1484
QY 255 rIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyVa 275
DB 1485 CGTGACCTTCACGCTACGCACTGGTGGTCCCGCATGTAGGAGCTGACCAACGTGCAGCA 1544

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RESULT 12
PCT-US94-08449A-3
; Sequence 3, Application PC/TUS9408449A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1 and 2
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449A
; FILING DATE: SUBMITTED HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA

```

PCT-US94-08449A-3

## Alignment Scores:

Pred. No.: 6,72e-69 Length: 2483  
Score: 635.00 Matches: 150  
Percent Similarity: 54.73% Conservative: 87  
Best Local Similarity: 34.64% Mismatches: 171  
Query Match: 28.67% Indels: 26  
DB: 5 Gaps: 9

US-10-016-647-2 (1-425) x PCT-US94-08449A-3 (1-2483)

QY 5 ArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAlaArgTyr 20  
DB 727 CAGAGCTCCCTGCCAGCGACGACATAGATAGTCTCAACGTGGGGCGGTGGCGGAG 786  
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40  
DB 787 GTGCTGTACGGGACCTCTCAGTCAGTACCTGACCGCGGTGGCGGAGCTCATCAAC 846  
QY 41 CysArgSer-----GluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58  
DB 847 TGTTCGTGGGGGTACGACACATCTTCCTCTGCGGAGCTACACCCCGGCAAG 906  
QY 59 AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArg 78  
DB 907 CGCGAGTTCTTTCACAGGACCGCGAGCGCTTCAAGTGTGTC---ATCGAGGTGTAC 963  
QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98  
DB 964 TATTTCCGGGAGTCCACATCAAGAGAGGACATCTGCCCATCTCTCAAGAACGAGATG 1023  
QY 99 IleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAsp 118  
DB 1024 GACTTCTGGAGGTGACCTCAAGTTCCTGGAGACTGTTCGAGAGCCACCTGAGCGAG 1083  
QY 119 ArgMetSerAspThrTyrThrPheTyrSer-----AlaAspGluProGlyValLeuGly 136  
DB 1084 AAGCGGAGAGCTGGAGGAGATCGC-GCGCCGCTGCAGCTCATCTCGGACGACTGGG 1142  
QY 137 ArgAspGluAlaArgProGlyAlaGluAlaAlaProSerArgArg-TripLeuGluArg 156  
DB 1143 CGTGGACGCGCGCA---GGCGCGTGGCGCGCTGCCAGAGTGTCTG-----1191  
QY 156 gMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerVa 176  
DB 1192 -----AAGTCTCTGAGAGACCGAGTGTCTGTCGCGCGCGGTGGTGGCGAGCT 1244  
QY 176 lSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspThr 196  
DB 1245 CTCCTTCCTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1304  
QY 196 pArgAsnAlaAlaAlaAsp---AsnArgSerLeuAspAspArgSerArgIleGluAl 215  
DB 1305 GCAGGTGCTGGAGCGCGGAGGACCGCGCTGGAGACCGCGCTGGAGAGCTGGAGAC 1364  
QY 215 alleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLy 235  
DB 1365 GCGGTGCATTTGGTGTGTCCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1424  
QY 235 sCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTy 255  
DB 1425 GCTGCATTCGCGCTCTCTCTCATGACATTTGGAGCGTGGCGATCTCTCTCTCTCTCT 1484  
QY 255 rIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyVa 275  
DB 1485 CBTGAGCTTCAGCTCAGCCACCTGGGTGGCGGATGATGGAGCTGACCAACGTCAGCA 1544  
QY 275 lThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisph 295  
DB 1545 GCGCGTGCAGGCTCGGATGATGCGGATCGCGGATCTTCAAGCTGGCGGCGCATC 1604  
QY 295 eIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLe 315

DB 1605 CTCGGGCTGCAGAGACCTCTCACCTATGCTTCAAGCGAGCTTCAAGGAACTGGGCTGCT 1664  
QY 315 uLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHi 335  
DB 1665 GCTCATGTACCTGCAGTGGGTATCTTCGTCTTCTTCTGCTG-----1707  
QY 335 sGlyLeuAspLeuGluThrSerAsnLysAsp-----PheThrSerIleProAlaAlaCy 353  
DB 1708 -GGCTACACCATGAGCAGAGCCATCCAGAGACCTCTTTAAGAACATCCCCAGTCTT 1766  
QY 353 sTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrVa 373  
DB 1767 CTGTGGCCATCATCACCATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1826  
QY 373 lProGlyArgIleLeuGlyValCysValSerGlyIleValSerGlyIleValLeuLeuAlaLeuPr 393  
DB 1827 GCTGAGCAAGCTCAACGCGGCGCATCAGCTTCTTGTGTGTGTGCTGCTGCTGCTGCTGCT 1886  
QY 393 oIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLysPheArgSerAl 413  
DB 1887 CATCCACCCATCATCAACAACTTTGTCAGTACTACAAAGAGCGCGCTCTCTGAGAC 1946  
QY 413 aArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425  
DB 1947 CGCGGCCAACGACGAGCTGGAGCTGATGGAACCTCAAC 1983  
RESULT 13  
US-10-162-012-7  
; Sequence 7, Application US/10162012  
; Patent No. 6682597  
; GENERAL INFORMATION:  
; APPLICANT: Curtiss, Rory A.J.  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS  
; FILE REFERENCE: 10448-190001  
; CURRENT APPLICATION NUMBER: US/10/162,012  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,845  
; PRIOR FILING DATE: 2000-06-06  
; PRIOR APPLICATION NUMBER: US 09/875,321  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: PCT/US01/18340  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/209,257  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: US 09/875,423  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: PCT/US01/18398  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/209,238  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: US 09/875,363  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: PCT/US01/18247  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/227,068  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: US 09/928,530  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/25475  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: US 60/226,770  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: US 09/934,421  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: PCT/US01/26096  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/279,281  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 10/109,029  
; PRIOR FILING DATE: 2002-03-28

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; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1338)
US-10-016-012-7

Alignment Scores:
Pred. No.: 1,38e-64 Length: 1341
Score: 597.00 Matches: 148
Percent Similarity: 51.76% Conserves: 73
Best Local Similarity: 34.66% Mismatches: 137
Query Match: 26.95% Indels: 70
DB: 4 Gaps: 10

US-10-016-647-2 (1-425) x US-10-162-012-7 (1-1341)

QY 11 ValValLeuAsnValGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe 30
DB 13 CTGGTGCTCAACGTGGCGGGCTCGCTTCAGACGGCGGGCGCGACGCTGGCGCGCTTC 72
QY 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
DB 73 CCG-----GACACTCTGTAGGGGACCCAGCGCGCGCGCTTC----- 114
QY 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
DB 115 -----TAGCAGCAGCGCGCGCGAGATTCTTCACCGGCACCGGCCAGCTTC 165
QY 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
DB 166 GAGCGGTGCTCTACTACCACTCCGTGGCGGTGGCGGGCGCGCGCGCGCGCGCTGC 225
QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
DB 226 CTCGACGTCTTCTCGGAAGAGGTGCCTTCTACGGGCTG----- 264
QY 111 CysCysGlnArgArgLeuAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
DB 265 -----GGCGCGCG- 272
QY 131 GluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaProSer 150
DB 273 GGCCCTGGCAGCCTCGCGAGGAGGAGGGGTGCCCGTGCCTGCCCGAGCGCCCTGCG 332
QY 151 -ArgArg---TrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuL 169
DB 333 CGCGCGCGCTTCGCGCCCGACGTGCGCTCTTCGATTTCCGAGAGCTCTCAGCG 392
QY 169 aAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeuCy 189
DB 393 CGCGCGGTGCTCGCGGTAGTCTCCGTGTGGTCACTCTCTCCATCGTCTGCTTCG 452
QY 189 sAlaSerThrLeuProAspTTrpArgAsn-----Al 199
DB 453 CCTCAGAGCGTGCCTGACTTCCGCGCAGCAGCGCGCGCGGGGCTTGTCTGTCTG 512
QY 199 aAlaAlaAsp-----AsnArgSer----- 205
DB 513 CGCAGCGCGCGCTTCCCGCTCCGCTCGAATGGCTTCAGCCAAATGCCTGGAATCCAC 572
QY 206 -----LeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheTh 222

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573 CGCGCTGCCCTTCAATGACCGCTCTCTCGTGGTGGAGACGCTGTGATTTGTTGTTCTTC 6332

222 rAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgPr 242

633 CTTTGAGCTCTGTGTAGCGCTCTCTGTCTGTCTCAAGCAAGGCTATCTTCAAGAACGT 692

242 oLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMetThrVa 262

693 GATGAACCTCAUGATTTTGTGGCTATCTTCCCTACTTTGTGGCA---CTGGGCACCGA 749

262 lPheThrGlyGluAsnSerGlnLeuGlnArgAlaGly-----ValThrLeuArgValle 280

750 GCTGGCCCGCAGCAGGAGGGGTGGCCGACGAGGCGCATGTCACGTGCCCATCTGTGAGTGCAT 809

280 uArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheIleGlyLeuGlnTh 300

810 CCGATTGGTGGCTGTCTTCCGCTATCTTAAGCTGTCCCGGCATCTCAAGAGGCCCTGCCAAT 869

300 rLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCy 320

870 CTTGGGCCAGACGCTTCCGGCCCTCCATGCGTAGCTGGGCTCCTCATCTTTTCTCTCT 929

320 sValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGl 340

930 CATCGGTGTGGTCTCTTTCCAGCGCGCTACTTTGCCGAA-----GTGA 977

340 uThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMe 360

978 CCGGGTGGACTCCCATTTCTACTAGCATCCCTGAGTCCTCTTGGTGGCGGTAGTCACCAT 1037

360 tThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGl 380

1038 GACTACAGTTGGCTATGGAGACATGGCACCGCTCACTGTGGTGGCGCAAGATAGTGGGCTC 1097

380 yValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSe 400

1098 TCTGTGTGCATTGGGGGTGTGTGACTATTTCCCTGCCAGTGCCTGCTCATTTGCTCTCAA 1157

400 rPheValGlnCysTyrHis 406

1158 TTTTCAGCTACTTTTATCAC 1176

RESULT 14

US-07-955-916-6

Sequence 6, Application US/07955916

Patent No. 5397702

GENERAL INFORMATION:

APPLICANT: CAHALAN, Michael D.

APPLICANT: CHANDY, Kanianthara G.

APPLICANT: GRISSMER, Stephen

APPLICANT: GHANSHANI, Sanjlu

APPLICANT: GUTMAN, George A.

APPLICANT: DETHLEFS, Brent A.

TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE

TITLE OF INVENTION: DISEASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/955,916

FILING DATE: 19921002

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:





; OTHER INFORMATION: K+Hnov4  
US-09-336-643A-3

Alignment Scores:

Pred. No.:	2.66-62	Length:	1927
Score:	581.00	Matches:	145
Percent Similarity:	49.89%	Conservative:	81
Best Local Similarity:	32.01%	Mismatches:	161
Query Match:	26.23%	Indels:	66
DB:	4	Gaps:	14

US-10-016-647-2 (1-425) x US-09-336-643A-3 (1-1927)

QY	7	GIyAlaLaSer-----ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArg	24
Db	114	GGCGAGGGCTCGGAGAAATCATATCAACGTGGCGGCACGGACATGAGACTACCGC	173
QY	25	GluLeuLeuLysAspPheProLeuArgArgValSerArgLeu-----HisGly	40
Db	174	AGCACCTTGGCGACCTACCGGGAAACCGCTCGCTGGCTGGCCGACCCCGAGCGGGG	233
QY	41	CysArgSerGluArgAspValLeuGluVal-----	50
Db	234	GGCCGGCGCCGAGACCGATGGCGGGCGGTGTGGGTAGCAGCGGCAGCAGCGCGCGGGCG	293
QY	51	CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe	70
Db	294	TGC-----GAGTCTCTTCGCACAGGCACCCGGCGCTCTTC	329
QY	71	GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys	90
Db	330	GCCTACGTGCTCAACTACTACCGC---ACCGGCAAGCTGCACCTGCCCGCAGACGTGTGC	386
QY	91	GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr	110
Db	387	GGCGCGCTCTTCGAGGAGGACTCGCTTCGGGGCATCGACGAGACCGACGTGGAGCC	446
QY	111	CysCys-----GluArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyr	127
Db	447	TGCTGCTGGATGACCTACCGCGCAGCACCGCGACGCCCGAGGCGCTGGACATCTTCGAG	506
QY	128	SerAlaAsp-----GluProGly-----ValLeu	135
Db	507	ACCCCGGACCTCATTTGGCGGGGACCCCGCGCAGCAGGACCTGGCGGCACAGAGCTG	566
QY	136	GlyArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgTyrTrpLeuGlu	155
Db	567	GCATCGAGGACGGCGGGGCTCGGGGGCCCCGACGGCAAACTGGCCCTGGAGGAGG	626
QY	156	-----ArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIle	172
Db	627	CTGCAGCCCGCATGTGGCGCTCTTCGAAGACCCCTACTCGTCCAGCGCGCCAGTTT	686
QY	173	LeuAlaSerValSerValValPheValIleValSerMetValValLeuCysAlaSerThr	192
Db	687	ATTGCTTTTGCTCTTTATTCTTCATCCGTTTCAATTACAACCTTTTTCCTGGAAACA	746
QY	193	-----LeuProAspTrpArgAsnAlaAlaAlaAspAsnArgSerLeu	206
Db	747	CATGAAGCTTTCAATATTGTTAAAAACAAGACAGAACCGATCATCATGCACAAGTGT	806
QY	207	-----AspAspArgSerArgIleIleGluAlaIleCysIle	218
Db	807	GTTCTACATGATAAATTGAAACGGATCTCTGCTTGACGTATGTAGAGGAGTGTGTG	866
QY	219	GlyTyrPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPhe	238
Db	867	GNIGTGTTTACTTTTGATTTTGTAGTCGGTATGTTTTTTCACCCCAATAACTTGATTC	926
QY	239	ValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerVal	258
Db	927	ATCAAAAAATCTCTGAATATCATGACTTTGTGGCATCTCCTACTCTTCTACTTAGAGTG	986

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GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2004, 14:00:02 ; Search time 576 Seconds  
(without alignments)  
3301.557 Million cell updates/sec

Title: US-10-016-647-2  
Perfect score: 2215  
Sequence: 1 MFGRSGAASVVLNVGGARY.....HELKFRSARYRSUSTEFLN 425

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh

-MODE=frames\_p2n.model -DEV=xlh  
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10016647 @CGN 1 1 472 @runat\_19042004\_104950\_10203  
-NCPU=6 -ICPU=3 -NO.MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
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Database : Published Applications NA:  
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15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*  
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19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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ALIGNMENTS

RESULT 1  
US-10-016-647-1  
; Sequence 1, Application US/10016647  
; Publication No. US20020160475A1  
; GENERAL INFORMATION:  
; APPLICANT: Fridde, Carl Johan  
; APPLICANT: Hilbun, Erin  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide

FILE REFERENCE: LEX-0284-USA  
CURRENT APPLICATION NUMBER: US/10/016,647  
CURRENT FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/257,932  
PRIOR FILING DATE: 2000-12-20  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1278  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-016-647-1

Alignment Scores:

1	2215	100.0	1278	14	US-10-016-647-1	Sequence 1, Appli
2	2215	100.0	1844	14	US-10-016-647-3	Sequence 3, Appli
3	2209	99.7	3215	15	US-10-199-869-1	Sequence 1, Appli
4	2035.5	94.6	1651	13	US-10-114-270-45	Sequence 45, Appli
5	2076.5	93.7	2235	16	US-10-415-378-39	Sequence 39, Appli
6	1028	46.4	594	15	US-10-199-869-26	Sequence 139, App
7	864.5	39.0	2370	10	US-09-971-392-139	Sequence 1, Appli
8	835.5	38.6	2127	14	US-10-143-002-1	Sequence 1, Appli
9	835.5	38.6	2127	15	US-10-325-891-1	Sequence 628, App
10	839.5	37.4	2499	15	US-10-101-510-628	Sequence 10, Appli
11	780.5	35.2	2565	13	US-10-435-935-10	Sequence 27, Appli
12	723.5	32.7	417	15	US-10-199-869-27	Sequence 7, Appli
13	715.5	32.3	3080	15	US-10-121-746-7	Sequence 2, Appli
14	685.5	30.9	1476	13	US-10-435-935-2	Sequence 1, Appli
15	685.5	30.9	2421	13	US-10-435-935-1	Sequence 5, Appli
16	685	30.9	2293	15	US-10-121-746-5	Sequence 17, Appli
17	683	30.8	3102	15	US-10-121-746-17	Sequence 439, App
18	683	30.8	5027	15	US-10-101-510-439	Sequence 827, App
19	667	30.1	3032	13	US-10-276-774-827	Sequence 25, Appli
20	661	29.8	461	13	US-09-852-386-25	Sequence 43, Appli
21	636.5	28.7	1455	13	US-10-114-270-43	Sequence 2, Appli
22	636.5	28.7	1638	13	US-09-833-466-2	Sequence 1, Appli
23	636.5	28.7	1871	10	US-09-918-359-1	Sequence 35, Appli
24	636.5	28.7	2103	13	US-09-999-220B-35	Sequence 5, Appli
25	636.5	28.7	2310	13	US-09-833-466-1	Sequence 3, Appli
26	636.5	28.7	2483	14	US-10-143-002-3	Sequence 119, App
27	635	28.7	2483	15	US-10-325-891-3	Sequence 1, Appli
28	635	28.6	1871	10	US-09-999-220B-119	Sequence 115, App
29	632.5	28.6	2850	10	US-09-999-220B-1	Sequence 7, Appli
30	632.5	28.6	2850	10	US-09-999-220B-115	Sequence 33, Appli
31	632.5	28.6	1747	13	US-09-804-014A-7	Sequence 1, Appli
32	600.5	27.1	1871	10	US-09-999-220B-33	Sequence 1, Appli
33	599.5	27.1	1871	10	US-09-999-220B-117	Sequence 3, Appli
34	599.5	27.1	1371	9	US-09-974-712-1	Sequence 1, Appli
35	599	27.0	1792	9	US-09-974-712-3	Sequence 3, Appli
36	599	27.0	4372	9	US-09-993-811-1	Sequence 3, Appli
37	599	27.0	4372	15	US-10-254-010-3	Sequence 16, Appli
38	599	27.0	6823	9	US-09-989-920-16	Sequence 7, Appli
39	597	27.0	1341	10	US-09-875-321-7	Sequence 7, Appli
40	597	27.0	1341	15	US-10-162-012-7	Sequence 7, Appli
41	597	27.0	1341	16	US-10-162-102-7	Sequence 20260, A
42	597	27.0	1341	15	US-10-029-386-20260	Sequence 1, Appli
c 43	596	26.9	1408	15	US-10-254-008-1	Sequence 7, Appli
c 44	594	26.8	5089	15	US-09-989-920-7	
c 45	593.5	26.8	777	9		

Pred. No.: 2,71e-277 Length: 1278  
 Score: 2215.00 Matches: 425  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-10-016-647-2 (1-425) x US-10-016-647-1 (1-1278)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyAlaAlaGlyTyr 20  
 Db 1 ATACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGTAACGTGGCGCGCCCGCGTAT 60  
 QY 21 SerLeuSerArgGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40  
 Db 61 TCCTGCTGCCGCGAGCTGCTGAAGGACTTCCTCGCGCGCGGTGAGCGCGGTGACGCGC 120  
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgGlu 60  
 Db 121 TGCCTGCTCCGAGCGCGACGTGCTCGAGGTGTCGACGACTACGACCGCGAGCGCAACGAG 180  
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80  
 Db 181 TACTTCTTCGACCGGCACCTCGAGGGCTTCGGCTTCATCTCTGCTCTACGTGCGCGCCAC 240  
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
 Db 241 GGCAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTCTTCTACAAACGAGATGATCTAC 300  
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgGluLeuAspArgMet 120  
 Db 301 TGGGGCTGAGGGCGGCGACCTCGAGTACTGCTGCGAGCGCGCTTCGACCGCGCATG 360  
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
 Db 361 TCCGACACCTTACACCTTCTACTCGCGCGAGCGCGGCTGCTGGCGCGCGAGCGG 420  
 QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgGlyThr 160  
 Db 421 CGCCCGCGCGGGCGGCGGCTGCTCGAGCGCTGCTGAGCGCATGCGCGGAC 480  
 QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180  
 Db 481 TTCGAGGAGCCACGCTCGTCTGCGCGCGAGCATCTGCTGCTAGCGTGTGCTGTTC 540  
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200  
 Db 541 GTGATCGTGTCCATGTTGGTGTGCTGCGCGAGCAGCTTGGCGAGCGCGCGCGCG 600  
 QY 201 AlaAspAsnArgSerLeuAspAspArgSerArgIleGlyAlaAlaCysIleGlyTyr 220  
 Db 601 GCGGACNACCGAGCGCTGGATGACCGGAGCAGGATTAATGAGCTATCTGATAGTTGG 660  
 QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240  
 Db 661 TTCCTGCTCCGAGTGCATGCTGAGGTTCAATGCTCCAAAACAAAGTGTGAGTTGTCAG 720  
 QY 241 ArgProLeuAsnIleLeuAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260  
 Db 721 AGACCCCTGAAACATCATGATTTACTGGGCTATGAGGCTGAGGCTGAGGCTGAGG 780  
 QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280  
 Db 781 ACAGTGTTCACGCGGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGAGGTACTT 840  
 QY 281 ArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300  
 Db 841 AGAATGATGAGGATTTTGGGAGTATGAGCTTGGCCGCTCATCTTCACTTCTTACACA 900  
 QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320  
 Db 901 CTCGGTTTGACTCTCAAAACGCTGCTACCGAGAGATGGTTATGTTACTTGTCTTCTTGT 960

RESULT 2

US-10-016-647-3  
 ; Sequence 3, Application US/10016647  
 ; Publication No. US20020160475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fiddle, Carl Johan  
 ; APPLICANT: Hilbun, Erin  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; FILE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide  
 ; TITLE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide  
 ; CURRENT APPLICATION NUMBER: US/10/016,647  
 ; CURRENT FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/257,932  
 ; PRIOR FILING DATE: 2000-12-20  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1844  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-016-647-3

Alignment Scores:  
 Pred. No.: 5e-277 Length: 1844  
 Score: 2215.00 Matches: 425  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-10-016-647-2 (1-425) x US-10-016-647-3 (1-1844)

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 Db 457 ATGACCTTCGGCGCAGCGCGGCGGCTCGGTGCTGCTGAACGTGGCGCGCCCGGTAT 516  
 QY 21 SerLeuSerArgGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40  
 Db 517 TCCTGCTCCCGGAGCTGCTGAAGGACTTCCTCGCTGCGCGCGGTGAGCCGGCTGCACGGC 576  
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgGlu 60  
 Db 577 TGCCGCTCCGAGCGCGAGCTGCTCGAGGTGTCGACGACTACGACCGCGAGCGCAACGAG 636  
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80  
 Db 637 TACTTCTCGACCGGACCTCGAGGCTTCGGCTTCACTGCTCTACGTGCGCGGCGCAC 696  
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100

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Db 697 GGCAAGCTGGCTTCGCGCGGGATGTGCGAGCTCTCTTACACAGATGATCTAC 756
Qy 101 TrpGlyLeuGluAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
Db 757 TGGGGCTTGAGGGCGCGCACTCGAGTACTGCTGCCAGCGCGCTCGACACCGCATG 816
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 817 TCCGACACCTACACCTTCTACTTCGCGCGAGCGGGGTGCTGGCGCGCGAGGGG 876
Qy 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrTrpLeuGluArgMetArgThr 160
Db 877 CGCCCCGGGGCGCGAGCGGCTCCCTCCAGCGCTGGCTGAGCGCATGGCGGAC 936
Qy 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
Db 937 TTCGAGAGCCACGTCGTCGTCGGCGCGCAGATCTCTGGCTAGCGTTCGGTGTTC 996
Qy 181 ValIleValSerMetValValLeuGluCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
Db 997 GTGATCGTGTCCATGCTGTGTGTGCGCGCAGCAGCTTCCCGAGCTGGCGCAACGACGC 1056
Qy 201 AlaAspAsnArgSerLeuAspArgSerArgIleLeuAlaIleCysIleGlyTrp 220
Db 1057 GCGGACACCGCAGCTGTGATACCGGAGCAGGATAATTGAAGCTATCTGCATAGTTGG 1116
Qy 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
Db 1117 TTCACCTGCGAGTGATGCTGTGAGTTCAATTGCTCCAAAACAAGTGTGAGTTTGTCAAG 1176
Qy 241 ArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
Db 1177 AGACCCCTGAAATCATTAATTACTTGGCAATCAGCCGATATATACATCTCTGTGTGATG 1236
Qy 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
Db 1237 ACAGTGTTTACAGCGAGAACTCTCACTCCAGAGGCTGGAGTCACTTGGAGGTACTT 1296
Qy 281 ArgMetMetArgIlePheThrPheValLeuLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
Db 1297 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCCGTCACCTTCAATTGGTCTTCAGACA 1356
Qy 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuValPheIleCys 320
Db 1357 CTCGGTTTGACTCTCAAGCTTGCTACCAGAGATGGTTATGTTACTTCTTCATTGT 1416
Qy 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGlu 340
Db 1417 GTTGCCATGGCAATCTTTAGTCACCTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1476
Qy 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyrTrpValIleSerMet 360
Db 1477 ACATCCAAACAAGACTTTACCAAGCATTCCTGTCGCTGCTGGTGGTATATCTCTATG 1536
Qy 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380
Db 1537 ACTACAGTTGGCTATGGAGATATGATCTATATCAGATGCTCTGGAGAAATCTTGGAGA 1596
Qy 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
Db 1597 GTTGTGTGTGTGAGTGAATGTTCTATTGGCAATTTACCTATACATTTTATCTACCATAGC 1656
Qy 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
Db 1657 TTTGTGCACTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCC 1716
Qy 421 ThrGluPheLeuAsn 425
Db 1717 ACTGAATTCCTGAAT 1731
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RESULT 3

US-10-199-869-1

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/ Sequence 1, Application US/10199869
/ Publication No. US20030152953A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
/ TITLE OF INVENTION: K-alpha2
/ FILE REFERENCE: D0161 NP
/ CURRENT APPLICATION NUMBER: US/10/199,869
/ CURRENT FILING DATE: 2002-07-19
/ PRIOR APPLICATION NUMBER: US 60/306,577
/ PRIOR FILING DATE: 2001-07-19
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 3215
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1275)
/ OTHER INFORMATION:
US-10-199-869-1
Alignment Scores:
Pred. No.: 7,67e-276 Length: 3215
Score: 2209.00 Matches: 424
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 99.73% Indels: 0
DB: 15 Gaps: 0
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US-10-016-647-2 (1-425) x US-10-199-869-1 (1-3215)

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Qy 21 SerLeuSerArgGluLeuLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
Db 61 TCGCTGTCCCGGAGCTGTGAGGACTTCCCGCTGCGCGCGTGAAGCGCGCTCGACGGC 120
Qy 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
Db 121 TGGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGACGACTACGACCGCGAGCGCAACGAG 180
Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
Db 181 TACTTCTTCGACCGCGCAGCTCGGAGCGCTTCGGCTTCTATCCTGCTCTACGTGCGCGCAC 240
Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 241 GCGAAGCTGGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTAC 300
Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120
Db 301 TGGGGCTTGAGGGCGCGCACCTCGAGTACTGTGCTGCCAGCGCGCTCGACACCGCATG 360
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 361 TCCGACACCTTACACCTTCTACTCGCGCGAGCGGGCGTGTGGCGCGCATGCGGAGCGG 420
Qy 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr 160
Db 421 CGCCCCGGGGCGCGAGCGGCTCCCTCCAGCGCTGGTGGAGCGCATGCGCGGACGACC 480
Qy 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
Db 481 TTCGAGAGCGCGCAGCTGCTGCGCGCGCAGATCTCTGGCTAGCGGTGCGGTGTTTC 540
Qy 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
Db 541 GTGATGCTGTCCATGCTGTGTGTGCGCGCAGCAGCTTTCGCCGACTGGCGCAACGCGACGC 600
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QY 201 AlaAspAsnArgSerLeuAspArgSerArgGilellelualeCysleGlyTrp 220  
 DB 601 GCCGACACCGCAGCTGGATGACCGGAGCAGGATTAATGAAGCTATCTGCATAGTTGG 660  
 QY 221 PheThrAlaGluCysleValArgPheIleValSerIysAsnIysCysGluPheValIys 240  
 DB 661 TTCACGTCCGAGTGCATCGTGGGTTCTGTCCTCAAAACAAAGTGTGAGTTGCAAG 720  
 QY 241 ArgProLeuAsnIlelleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet 260  
 DB 721 AGACCCCTGAACATCATTTACTTGGCAATCAACGCGTATACATCTCTGTGTTGATG 780  
 QY 261 ThrValPheThrGlyGluLeuSerGlnLeuArgAlaGlyValThrLeuArgValLeu 280  
 DB 781 ACAGTGTTCACAGCGGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGGGTACTT 840  
 QY 281 ArgMetMetArgIlePheTTPValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300  
 DB 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCCGCTCACTTCATCTGCTTCAGATA 900  
 QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320  
 DB 901 CTCGGTTGACTCTCAACGCTTCTACCGAGAGATGTTATGTTACTTGTCTCTCTATTTGT 960  
 QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGlu 340  
 DB 961 GTTGCCATGGAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGCTGGACCTGGAA 1020  
 QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360  
 DB 1021 ACATCCAAAGACATTACCAACATTCCTGCTGCTGCTGGTGGGTGATTAATCTCTATG 1080  
 QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380  
 DB 1081 ACTACAGTTCGCTATGAGATATGTTATCCCTATCACAGTGCCTGGAGAAATTTCTGGAGA 1140  
 QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400  
 DB 1141 GTTTGTGTTGTCAGTGAATTTCTTATTGGCATTACCTATCACTTTTATCTACCATAGC 1200  
 QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420  
 DB 1201 TTTGTGAGTGTATCATGAGTCAAGTTTAGATCTGCTAGGTATAGTAGGACCTCTCC 1260  
 QY 421 ThrGluPheLeuAsn 425  
 DB 1261 ACTGAATTCCTGAAT 1275

RESULT 4

US-10-114-270-45  
 ; Sequence 45, Application US/10114270  
 ; Publication No. US20040030110A1  
 ; GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Malyankar, Uriel M.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Liu, Ziaohong  
 ; APPLICANT: Gusev, Vladimir Y.  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: zerhusen, Bryan D.  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Shimkets, Richard A.  
 ; APPLICANT: Gangolli, Esha A.

; APPLICANT: Taupier Jr., Raymond J.  
 ; APPLICANT: Caeman, Stacie J.  
 ; APPLICANT: Ji, Weizhen  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Lieste, Mario W.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Stone, David J.  
 ; APPLICANT: MacDougall, John R.  
 ; APPLICANT: Rothenberg, Mark E.  
 ; TITLE OF INVENTION: No. US20040030110A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-322C  
 ; CURRENT APPLICATION NUMBER: US/10/114,270  
 ; CURRENT FILING DATE: 2002-11-27  
 ; PRIOR APPLICATION NUMBER: 60/281,086  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,136  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,863  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,906  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/282,020  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/282,930  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/282,934  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/283,512  
 ; PRIOR FILING DATE: 2001-04-12  
 ; PRIOR APPLICATION NUMBER: 60/283,710  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/284,234  
 ; PRIOR FILING DATE: 2001-04-17  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 470  
 ; SEQ ID NO 45

; LENGTH: 1651  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1642)  
 US-10-114-270-45

Alignment Scores:

Pred. No.:	1,48e-261	Length:	1651
Score:	2095.50	Matches:	411
Percent Similarity:	91.54%	Conservative:	0
Best Local Similarity:	91.54%	Mismatches:	35
Query Match:	94.60%	Gaps:	3
DB:	13		

US-10-016-647-2 (1-425) x US-10-114-270-45 (1-1651)

QY	1	MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr	20
DB	58	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGTGTCTGAACGTGGCGGCCCGGTAT	117
QY	21	SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly	40
DB	118	TGCTGTCCCGGGAGCTCTGAGGACTTCCGCTGCGCGCGTGGCGGCTGACGGC	177
QY	41	CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu	60
DB	178	TGCCGCTCCGAGCGCAGCTGCTGAGGTGTGCGACACCTACGACCGCGGCGCAACGAG	237
QY	61	TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis	80
DB	238	TACTTCTTCGACCGGCACTCGAGGCCCTTCGGCTTCATCTGCTCTACGTGGCGGCCAC	297
QY	81	GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr	100

```

Db 298 GCAAGCTGCGCTTCGCGCCGCGGATGTCGAGCTCTCTTCTACAAAGAGATGATCTAC 357
Qy 101 TTPGlyLeuGluGlyValAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
Db 358 TGGGCGCTGGAGGGCGCGACCTCGAGTACTGCTGCCAGCGCGCTCGACACCGCATG 417
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 418 TCCGACACTACCTTCTACTCGCCGACGAGCGCGCGTCTGGGCGCGGAGCGGCG 477
Qy 141 ArgProGly-----GlyAlaGluAlaAlaPro--- 149
Db 478 CGCCCCGCGCGGAGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATCGCGCGACCTT 537
Qy 150 -----SerArgArgTrpLeuGluArgMetArgArgThrPhe 161
Db 538 CGAGGAGCCACGCTCGCTCGCTGGCCGCGAGCGCTGGCTGGAGCGCATCGCGCGACCTTC 597
Qy 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPheVal 181
Db 598 GAGGAGCCACGCTCGCTCGCGCCGCGAGATCTCGCTAGCGTGTGCGTGTGCTG 657
Qy 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 201
Db 658 ATCGTGTCCATGTTGGTGTGTGCGCCAGCAGCTTGCCCGACTGGCGCAACGCGCGCC 717
Qy 202 AspAsnArgSerLeuAspArgSer----- 210
Db 718 GACAAACCGAGCCTGGATGACCGGAGCAGGACTCCGCGCGCCCTGGAGGAGCGCCCTCC 777
Qy 211 -----ArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCys 225
Db 778 GGGTGTCTCTTGACAGGATAATGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGC 837
Qy 226 IleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIle 245
Db 838 ATCGTGAGGTTCATTGTCTCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATC 897
Qy 246 IleAspLeuLeuAlaIleThrProTyrTrpIleSerValLeuMetThrValPheThrGly 265
Db 898 ATTGATTTACTGGCAATCAGCCGATTCATCTCTGTGTGTGATGACAGTGTTCACAGGC 957
Qy 266 GluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle 285
Db 958 GAGAACTCTAACTCCAGAGGCTGAGTCACTTGGAGGTACTTAGAATGATGAGGATT 1017
Qy 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrIeu 305
Db 1018 TTTTGGGTGATTAAAGCTTGGCCGTCCTCATTTGCTCTTCAGACACTCGGTTTGACTCTC 1077
Qy 306 LysArgCysTyrArgGluMetValMetLeuValPheIleCysValAlaMetAlaIle 325
Db 1078 AAACGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCAITTTGTTGCCATGCAATC 1137
Qy 326 PheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345
Db 1138 TTTAGTGCACTTTCTCAGCTCTTGAACATGGGCTGGACCTCGGAACATCCAAACAGGAC 1197
Qy 346 PheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyr 365
Db 1198 TTTACAGCAATCTCTGCTGCTGCTGGTGGTGTATCTCTATGACTACAGTTGGCTAT 1257
Qy 366 GlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGlyValCysValValSer 385
Db 1258 CGAGATATGATATCTATCAGTGGCTCGAAGAAATCTTGGAGGAGTTTGTGTTCAGT 1317
Qy 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405
Db 1318 GGAATGTTCTATTGGCATTTACTTATCTTTTATCTACCATGCTTTTGTGAGTGTTAT 1377
Qy 406 HisGluLeuLysPheArgSerAlaArg 414
Db 1378 CATGAGCTCAAGTTTAGATCTGCTAGG 1404

```

## RESULT 5

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US-10-415-378-39
; Sequence 39, Application US/10415378
; Publication No. US20040014945A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom
; APPLICANT: YUE, Henry; NGUYEN, Dannie B.;
; APPLICANT: HAFALIA, April J.A.; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
; APPLICANT: GANDHI, Ameena R.; DING, Li;
; APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
; APPLICANT: ARVIZU, Chandra S.; GIETZEN, Kimberly J.;
; APPLICANT: LAL, Preeti G.; AZIMZAI, Raica;
; APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;
; APPLICANT: THIBOULEY, Michael B.; LU, Dyoung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
; APPLICANT: ISON, H. Craig; DAS, Debopriya;
; APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0270 USN
; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,661
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040014945A1 7482060CBI
US-10-415-378-39

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## Alignment Scores:

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Pred. No.: 7,28e-259 Length: 2235
Score: 2076.50 Matches: 406
Percent Similarity: 97.83% Conservative: 0
Best Local Similarity: 97.83% Mismatches: 1
Query Match: 93.75% Indels: 9
DB: 16 Gaps: 2

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US-10-016-647-2 (1-425) x US-10-415-378-39 (1-2235)

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Qy 1 MetThrPheGlySerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
Db 428 ATGACCTTCGGGCGCAGCGGGCGGCTCGTGTGCTGAACTGGCGCGCCCGGTAT 487
Qy 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
Db 488 TCGGTGTCCCGGAGCTGTCTGAAGGACTTCCCGCTGCGCGCTGAGCGGCTGCACGGC 547
Qy 41 CysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGlu 60
Db 548 TGCCTGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGACACTACGACCGGAGCGCAACGAG 607
Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80

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; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/009,492  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: 08/464,340  
 ; FILING DATE: June 5,1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FERRARO, GREGORY D.  
 ; REGISTRATION NUMBER: 36,134  
 ; REFERENCE/DOCKET NUMBER: 325800-415  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-994-1700  
 ; TELEFAX: 201-994-1744  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2127 BASE PAIRS  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: SINGLE  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: cDNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-10-325-891-1

Alignment Scores:  
 Pred. No.: 5,18e-100 Length: 2127  
 Score: 855.50 Matches: 178  
 Percent Similarity: 60.94% Conservative: 81  
 Best Local Similarity: 41.88% Mismatches: 141  
 Query Match: 38.62% Indels: 25  
 DB: 15 Gaps: 8

US-10-016-647-2 (1-425) x US-10-325-891-1 (1-2127)

QY 11 ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLeuAspPhe 30  
 DB 474 ATCATCATCAAGTATAGGGGATCAAGTACTCGCTGGCCCTGGACCAACGAGATTC 533  
 QY 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuVal 50  
 DB 534 CGCTGACGCGCTGGCGGAGCTCAAGCGCTCAACCACTTCGACGACATCTCAACGTG 593  
 QY 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70  
 DB 594 TCGGATGACTACGACGTACCTGCAACGAGTCTCTTCGACCGCAACCGGGGCTTC 653  
 QY 71 GlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90  
 DB 654 GGCACATATCTGACCTTCTGCGCGCG--GCAAGCTGCGGCTGCTGCGGAGATGTGC 710  
 QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110  
 DB 711 GCGTGTCTTCCAGGAGGAGTGTGTACTGGGCGATCGCGGAGACCACTGGACGCG 770  
 QY 111 CysCysGlnArgArgLeuAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130  
 DB 771 TGTGCAAGCGCGCTACCTGCAGAAGATTGAGGAGTTCGCGAGATGTTGGAGCGGAG 830  
 QY 131 GluProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGlu 146  
 DB 831 GAAGAGGACGACGCGCTGACAGCGAGGCGCCGCGACGACGAGCGCGCGCGAGCGGAG 890  
 QY 147 AlaAlaProSerArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSer 166  
 DB 891 GCGCGCTGGGG--CGCTGCATCGCGGACGTGCGGACATGCGGACATGCGGACGCG 947  
 QY 167 SerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetVal 186  
 DB 948 GGGCTGCGCTGGCAAGGTGTTCGCTGCTCGGCTCTTCGTCGACCTCACCGCGCTC 1007  
 QY 187 ValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArg----- 204  
 DB 1008 AACCTTCGCTCAGACACTTGCACCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1067  
 QY 205 SerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224

DB 1068 CAGATGTGCCAACACGTCCTTCATCGTGGAGTCGGTGTGGTGGCTGGTTCCTCCCTGGAG 1127  
 QY 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244  
 DB 1128 TTCCTCTCGTGGGTCAATTCAGGCGCCAGCAAGTTCGCTCTCTGGGAGCCGCTGACG 1187  
 QY 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThr---ValPhe 263  
 DB 1188 CTGATCGACCTGTGGCCATCTCGCTACTACTATACACGCTGCTGTGGAGCGCGCGCC 1247  
 QY 264 ThrGlyGlu-----AsnSerGlnLeuGlnArgAlaGlyValThrLeu 277  
 DB 1248 GCAGGCGCTGCAAGCCCGCGCGGCAACAGCTACTCTGGACAGGTGGGGCTGGTGTG 1307  
 QY 278 ArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGly 297  
 DB 1308 CGCTGTCTGGGCGCTGGCACTCTGTAGTGTGCGCTGGCGGCGCACTCCCTGGGG 1367  
 QY 298 LeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuVal 317  
 DB 1368 CTGCAGACGCTGGGCTCACGGCCGCGCTGCACCGCGAGTTCGGGCTCTCTGCTGCTC 1427  
 QY 318 PheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeu 337  
 DB 1428 TTCCTGTGCTGGCATCGCCCTCTTCGCGCCCTGCTTACGTCAFCGAGACGAGATG 1487  
 QY 338 AspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIle 357  
 DB 1488 -----GCCGACAGCCCGAGTTCACCGACATCTCTCCCTGCTACTGCTGGGCTGTC 1538  
 QY 358 IleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIle 377  
 DB 1539 ATCACCATGACGAGGTGGACTATGGCGACATGTCCTCCAGGAGCACCCCGGCGCAGGTA 1598  
 QY 378 LeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIle 397  
 DB 1599 GTGCCCTGAGCAGCATCTGAGCGGATCTCTGCTATGSCCTTCCAGTCCACTCCATC 1658  
 QY 398 TyrHisSerPheValGlnCysTyrHisGluLeuLys-----Phe 410  
 DB 1659 TTCACACCTTCTCCCGCTCTACCTGGAGCTCAACAGGAGCAAGAGAGGTGATGTTTC 1718  
 QY 411 ArgSerAlaArgTyr 415  
 DB 1719 CGGAGCGCGAGTTC 1733  
 RESULT 10  
 ; US-10-101-510-628  
 ; Sequence 628, Application US/10:01510  
 ; Publication No. US20030148295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WAN, JACKSON  
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
 ; FILE REFERENCE: 15117.0012  
 ; CURRENT APPLICATION NUMBER: US/10/101,510  
 ; PRIOR FILING DATE: 2002-03-20  
 ; PRIOR FILING DATE: 2001-03-20  
 ; NUMBER OF SEQ ID NOS: 805  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 628  
 ; LENGTH: 2499  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-101-510-628  
 Alignment Scores:  
 Pred. No.: 1.64e-96 Length: 2499  
 Score: 829.50 Matches: 181  
 Percent Similarity: 57.49% Conservative: 80  
 Best Local Similarity: 39.87% Mismatches: 138

[illegible]

Score: 780.50 Matches: 172  
Percent Similarity: 60.00% Conservative: 83  
Best Local Similarity: 49.47% Mismatches: 160  
Query Match: 35.24% Indels: 12  
DB: 13 Gaps: 5

US-10-016-647-2 (1-425) x US-10-435-935-10 (1-2565)

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QY 1 MetThrPheGlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAla 18
DB 49 ATGGAGATCGTCGGCAGCAAGCGGTCTCTGGCGGGTCCGCCCTCAACGTCGGGGGGCTG 108
QY 19 ArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeu 38
DB 109 GCGCAGGAGTACTCTGGGTACCCCTGACCGCCCTGCCCGCCGCGCGCTGGCAAGCTC 168
QY 39 HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58
DB 169 CCGCATCGCAACACGACGACATCGCTGCTCGAGGTGTCGATGACTACAGCCTCGAGC 228
QY 59 AsnGluTyrPhePheAspHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArg 78
DB 229 AACGAGTACTCTTTGACCGCCACCGCGCGCTTCACCTCCATCCTCAACTTCTACCGC 288
QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98
DB 289 ---ACTGGCGACTCCACATGATGGAGGAGATGTGCGCGCTCAGCTTCAGCCAAAGAGCTC 345
QY 99 IleTyrTPGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAsp 118
DB 346 GACTACTGGGCATCGACGAGTACTCTGAGTCTGCTGCCAGCGCCGCTACCAACG 405
QY 119 ArgMetSerAspThrTyrPheTyrSerAlaAspGluProGlyValLeuGlyArgAsp 138
DB 406 AAGAAAGACGACATGA--ACGAGGAGCTCAAGCGTGAGCGCGAGACTCTACGCGAGCGG 463
QY 139 GluAlaArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArg 158
DB 464 AAGCGGAGGAGTTCGATTAACAGTCTCGCA--GAGAAGAGG-----AAAAAAGTCTGG 516
QY 159 ArgThrPheGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerVal 178
DB 517 GACCTACTGGAGAGCCCAATTCCTCTGTGGTGCCAAAGATCCTTGCCATAATTTCCATC 576
QY 179 ValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsn 198
DB 577 ATGTTTCATCGTCTCTCCACCATTCCTCTGTCCTCAACACGCTGCGCTGAGCTACAGAGC 636
QY 199 AlaAlaAlaAspAsnArgSerLeuAspAsp---ArgSerArgIleGluAlaIleCys 217
DB 637 CTCGATGAGTTCGGCCAGTCCACACACACCCCAAGCTGGCCCGCTGGCGCGGTGTGC 696
QY 218 IleGlyTyrPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGlu 237
DB 697 ATCGCATGTTTCCACATGAGTACCTGTGTGAGTTCTCTCTCTGCCCAAGAGTGAAG 756
QY 238 PheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSer 257
DB 757 TTCCTCAGAGGCCCACTCAATGCCATGACTGTGTGGCCATCTGCCATATATGTACCC 816
QY 258 ValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeu 277
DB 817 ATTTTCTCACCAGTATCAACAAAGAGCGTGTGTGCAATTCAGATGTCCCGCGGTGTGC 876
QY 278 ArgValLeuArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheIleGly 297
DB 877 CAGATCTTCGGCATCATCGCAATTCGCGCATCTTAAGCTGTGACGCGCATCCACTGGC 936
QY 298 LeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuVal 317
DB 937 CTCAGTCTCTGGGTCTCATTGCGGAGGAGCTACATGAGTTGGGTCTGCTCATCTC 996
QY 318 PheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeu 337
```

```
DB 997 TTCCTTGCCATGGGCATTATGATCTTCTCAGCCTTGTCTTCTTGTGAGAAGGATGAG 1056
QY 338 AspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyrTrpValIle 357
DB 1057 GAC-----GACACCAAGTTCAAAGCATCCAGCCTCTTTCTGGTGGGCCACC 1104
QY 358 IleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIle 377
DB 1105 ATCACCATGACTACTGTTGGTATGGAGACATCTACCCCAAGACTCTCTCTGGGGAAT 1164
QY 378 LeuGlyCysValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIle 397
DB 1165 GTTGGGGAGCTGCTGCTCATTCGAGGATGCTGCTGATGCTCTTCCCATCCCATCATC 1224
QY 398 TyrHisSerPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArg 417
DB 1225 GTCAATTAATCTCTGAGTTCTATAGGACGACAGAGACAGGAGAAGCAATCAACCG 1284
QY 418 SerLeuSerThrGlu 422
DB 1285 CGAGAGGCTCTGGAG 1299

RESULT 12
US-10-199-869-27
; Sequence 27, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUBI
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-27

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Score: 723.50 Matches: 138
Percent Similarity: 98.57% Conservative: 0
Best Local Similarity: 98.57% Mismatches: 0
Query Match: 32.66% Indels: 2
DB: 15 Gaps: 1

US-10-016-647-2 (1-425) x US-10-199-869-27 (1-417)
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DB 61 CCCTGCGCGCGGTGAGCGCGCTGCACGCTGCCGTCCGAGCGCGACGTCGCGAGGTG 120
QY 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
DB 121 TGGACGACTACACCGCGAGCGCACAGAGTACTTCTCGACCGGCACTCGGAGGCTTC 180
QY 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
DB 181 GGCTTTCATCTGCTACGTGCGCGCGCCACGCAAGCTGCGCTTCGCGCGCGAGTGTGC 240
QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGluAlaHisLeuGluTyr 110
DB 241 GAGCTCTCTCTACACAGAGATGATCTACTGGGGCTTGAGGCGCGGACCTCGAGTAC 300
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US-10-435-935-2
; Sequence 2, Application US/10435935
; Publication No. US20040038890A1
; GENERAL INFORMATION:
; APPLICANT: Aiyar, Jayashree
;            Kang, Jiesheng
; TITLE OF INVENTION: HUMAN VOLTAGE-GATED POTASSIUM
;                   CHANNEL SUBUNIT
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Pharmaceuticals, Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850-5437
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/435,935
; FILING DATE: 12-May-2003
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,878
; FILING DATE: 08-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Higgins, Patrick H
; REGISTRATION NUMBER: 39,709
; REFERENCE/DOCKET NUMBER: PHM.70310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302.886.4889
; TELEFAX: 302.886.8221
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1476 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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QY 35 ValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAsp 54
Db 121 CTGGGAAGCTGCTTACTTCTGCAATCTGGAAGAGGCCATCTGGAGCTGTGATAT 180
QY 55 AspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPhe 74
Db 181 AGTGTGGCCGATPAGGAATACTACTTTGATCGAATCCCTCTTGTTCAGATATG 240
QY 75 LeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeu 94
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298 TGCAGGAGATCAGTACTGGGCGCATCAACGAGCTCTTCATTGATCTTCTGTCGACCAAT 357
115 ArgLeu-----AspAspArgMetSerAsp 122
358 CGCTACAGGAACGCAAGGAGGAAACACACGAGAGGACTGGGACCCAGAAAGCCATGAT 417
123 ThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArg----- 137
418 GTGAGTACCGACTCCCTCTGTTGAAGAGTCTGCTCTGTTGAGAAAGAGCTGGAGAAGTTT 477
138 AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTyrLeuGluArgMet 157
478 GACACACTGCGATTTCGTCAGCTCCGG-----AAGAAATATCGGATTAGA----- 522
158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGluLeuLeuAlaSerValSer 177
523 -----ATGGAGAAATCCAGCGTACTCGCTGTCGCTAAGCTTATCGTATATCTCTCC 573
178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
574 TTGAGCGTGTGCTGGCTCCATCGTGGCCATGTGGTTCACAGCATGTCCGAGTTCCAG 633
198 AsnAlaAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleleGluAlaIle--- 216
634 AAT-----GAGGATGAGAGGATGATGAT-----CCGGTGTGGAAGAGGTGGAG 678
217 -----CysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsn 234
679 ATCGGTGTCATTCGCTGTTTACCGGGAGCTTGGCGTCCGGTGGCTCCGCTCTCTGT 738
235 LysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyr 254
739 CAAAGAAATTCGGAAACCCCTCTGAACATCATTTGCTCTATTATTCTCTCTTC 798
255 TyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGluAlaGly 274
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295 PheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet 314
919 TCGGTAGGACTTCGGTCTCTAGTGGCCACTGACACACAGCTACCATGAAGTTGGCGCT 978
315 LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGlu 334
979 CTGCTTCTCTCTCTCTCTGTCGTCATTTCCATTTTCTCTGCTTATCTACTCCGTGGAG 1038
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1039 AAA-----GATGACACACATCCAGC-----CTCACCAGCATCCCATCTCTGTTGG 1086
355 TrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValPro 374
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375 GlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIle 394
1147 GGAAGCTCATCGCCAGCACATCATCTGTGGCATCTTGTGGTGGTGGCTTCCCATC 1206
395 ThrPheIleTyrHisSerPheValGlnCysTyr----- 405
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Job time : 640 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2004, 12:51:52 ; Search time 4330 Seconds  
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3453.603 Million cell updates/sec

Title: US-10-016-647-2

Perfect score: 2215

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Total number of hits satisfying chosen parameters: 75154660

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
Db 781 ACAGTGTTTACAGGCGAGAACCTCAACTCCAGAGGGCTGGAGTCACCTTGAGGGTACTT 840
QY 281 ArgMetMetArgIlePheThrValIleLeuAlaArgHisPheIleGlyLeuGlnThr 300
Db 841 AGAAATGATGAGGATTTTGTGGTGATTAAGCTTGCCCGTCACTTCATTGGTCTTCAGACA 900
QY 301 LeuGlyLeuThrLeuLeuArgCysTyrArgGluMetValMetLeuValPheIleCys 320
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QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGlu 340
Db 961 GTTGCCATGGCAATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGGCTGACCTGGAA 1020
QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyrTyrValIleIleSerMet 360
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QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGly 380
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QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
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QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaAlaArgTyrSerArgSerLeuSer 420
Db 1201 TTTGTGCACTTATCATGAGCTCAAGTTTAGATCTGCTAGTATAGTAGGAGCCTCTCC 1260
QY 421 ThrGluPheLeuAsn 425
Db 1261 ACTGAATTCCTGAAT 1275

RESULT 2
US-10-016-647-3
; Sequence 3: Application US/10016647
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0284-USA
; CURRENT APPLICATION NUMBER: US/10/016,647
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/257,932
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-016-647-3
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Score: 2215.00 Matches: 425
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 43 Gaps: 0
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US-10-016-647-2 (1-425) x US-10-016-647-3 (1-1844)

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QY 201 AlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTyr 220
Db 1057 GCCGACAAACCGCGAGCTGGATGACCGGAGGAGATATTTGAAGCTATCTCATGTGTG 1116
QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
Db 1117 TTCCTGCCGAGTGATCTGAGGTTCATTTCTTCCAAAACAAAGTGTGAGTTGTCAAG 1176
QY 241 ArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
Db 1177 AGACCCCTGAAACATCA-TGATTTTACTGGCAATCAGCGCGTATTACATCTCTGTGTG 1236
QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
Db 1237 ACAGTGTTCAGCGGAGAACTCTCAACTCCAGAGGGCTGGAGTCACCTTGAGGGTACTT 1296
QY 281 ArgMetMetArgIlePheTyrValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
Db 1297 AGAATGATGAGATTTTGGGTGATTAAAGTTCGCCGCTCATTCTTGTCTTCAGACA 1356
QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
Db 1357 CTCGGTTTGACTCTCAAAACGTGTGCTACCGAGAGATGGTTATGTACTTGTCTTCATTGT 1416
QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340
Db 1417 GTTCCCATGGCAATCTTTAGTGCATTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1476
QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMet 360
Db 1477 ACATCCAAACAGGACTTTACAGCATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1536
QY 361 ThrThrValGlyTyrGlyArgMetTyrProIleThrValProGlyArgIleLeuGly 380
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;; PRIOR APPLICATION NUMBER: US 60/306,577  
;; PRIOR FILING DATE: 2001-07-19  
;; NUMBER OF SEQ ID NOS: 90  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1  
;; LENGTH: 3215  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(1275)  
;; OTHER INFORMATION:  
US-10-199-869-1

## Alignment Scores:

Pred. No.: 5,62e-218 Length: 3215  
Score: 2209.00 Matches: 424  
Percent Similarity: 99.76% Conservative: 0  
Best Local Similarity: 99.76% Mismatches: 1  
Query Match: 99.73% Indels: 0  
DB: 46 Gaps: 0

US-10-016-647-2 (1-425) x US-10-199-869-1 (1-3215)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyAlaArgTyr 20  
DB 1 ATGACCTTCGGCGCGAGCGGGCGCTCGGTGGTGTCTGAACGTCGGCGCGCGCGGTAT 60  
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40  
DB 61 TCGCTGTCCGGAGAGTGTCTGAAGACTTCCCGCTGCGCGCGGTGAGCGGCTGACCGC 120  
QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
DB 121 TCCCGCTCCAGCGCGAGCGTGTCTGAGGTGTGCGAGCTACGACCGCGAGCGCACGAG 180  
QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80  
DB 181 TACTTCTTCGACCGGCACCTTCGAGGCGCTTCGGCTTCATCTCTCTACGTGCGCGCCAC 240  
QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
DB 241 GCGAGCTCGCTTCGCGCGCGAGTGTGCGAGCTCTCTCTTCAACGAGATGATCTAC 300  
QY 101 TrpGlyLeuGluAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120  
DB 301 TGGGGCTCGAGCGCGCACCTCGAGTACTGCTGCCAGCGCGCTCGACGACGCGATG 360  
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
DB 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGCGGTGCTGCGCGCGAGCGCG 420  
QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrTrpLeuGluArgMetArgTyr 160  
DB 421 CGCCCGCGCGCGCGAGCGCTCCCTCCAGCGCGCTGGCTGAGCGCATCGCGCGGACC 480  
QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnLeuLeuAlaSerValSerValPhe 180  
DB 481 TTCGAGGACCCACCGCTGCTGCTGCGCGCGAGATCTCGCTGAGCGTGTGCTGCTTC 540  
QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200  
DB 541 GTGATCGTGTCTCATGTGTGTGTGCGCACACAGTGTCCCGCATGGCGCACCGACCC 600  
QY 201 AlaAspAsnArgSerLeuAspArgSerArgIleGluAlaIleCysIleGlyTyr 220  
DB 601 GCCGACACCGCGCGCTGATGACCGAGCAGGATAATTGAAGCTATCTGCATAGTTGG 660  
QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240  
DB 661 TTCACGCGCGATGATCGTGAAGTTCATGTCTCCAAAAACAAGTGTGAGTTGTCAAG 720  
QY 241 ArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet 260

DB 721 AGACCCCTGAACATCATTTACTGCGCAATCAAGCGGTATTACATCTCTGTGTGATG 780  
QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGluArgAlaGlyValThrLeuArgValLeu 280  
DB 781 ACAGTGTTCAGCGCGAGAACTCTCAACTCCAGAGGCTGAGTCACTTGAGGCTACTT 840  
QY 281 ArgMetMetArgIlePheTyrValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300  
DB 841 AGAATGATGAGGATTTTGGGTGATTAAAGCTTCCCGTCACTTCATTTGCTTCAGATA 900  
QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320  
DB 901 CTCGGTTTACTCTCAACCGTTGCTACGAGAGATGGTTATGTTACTTGTCTTCATTGT 960  
QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340  
DB 961 GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGCGTGGACCTGAA 1020  
QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360  
DB 1021 ACATCCAAACAGGACTTTACAGCATTCCTGCTGCTGCTGGTGGTATTATCTCTATG 1080  
QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380  
DB 1081 ACTACAGTTGGCTATGGAGATATGTAATCTATCACAGTGCCTGGAAGAAATCTTGGAGGA 1140  
QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400  
DB 1141 GTTTGTGTGTGAGTGAATTTCTTATTTGCACTTACCTATCACTTTATCTACCATAGC 1200  
QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420  
DB 1201 TTTTGTGAGTGTATCATGAGCTCAAGTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1260  
QY 421 ThrGluPheLeuAsn 425  
DB 1261 ACTGAATTCCTGAAT 1275

## RESULT 5

US-60-306-577-1

; Sequence 1, Application US/60306577

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB

; FILE REFERENCE: K+alphaM2

; CURRENT APPLICATION NUMBER: US/60/306,577

; NUMBER OF SEQ ID NOS: 40

; CURRENT FILING DATE: 2001-07-19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3215

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1275)

US-60-306-577-1

## Alignment Scores:

Pred. No.: 5,62e-218 Length: 3215  
Score: 2209.00 Matches: 424  
Percent Similarity: 99.76% Conservative: 0  
Best Local Similarity: 99.76% Mismatches: 1  
Query Match: 99.73% Indels: 0  
DB: 87 Gaps: 0

US-10-016-647-2 (1-425) x US-60-306-577-1 (1-3215)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyAlaArgTyr 20  
DB 1 ATGACCTTCGGCGCGAGCGGGCGCTCGGTGGTGTCTGAACGTCGGCGCGCGCGGTAT 60



Qy 41 CysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGlu 60  
 Db 547 TCGCGCTCCGAGCGGACGCTGCTCGAGGTGTGCGACGACTACGACCGGAGCGAACGAG 606  
 Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80  
 Db 607 TACTTCTTCGACCGGACCTCGAGGCGCTTCGGCTTCCTCCCTGCTACGTGCGGCGCAC 666  
 Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
 Db 667 GSCAAGCTCGCTTCGCGCGCGGAGTGTGCGAGCTCTCTTCTACACGAGATGATCTAC 726  
 Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120  
 Db 727 TGGGGCCTTGAGGGCGCGACCTCGAGTACTGCTGCCAGCGCGCTCGAGCGCGCATG 786  
 Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
 Db 787 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGGCGTGTGCGCGGAGCGGCG 846  
 Qy 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgArgThr 160  
 Db 847 CGCCCGCGGCGGCGGCGGCTCCCTCCAGCGCTGCTGCGAGCGCATCGCGCGGAC 906  
 Qy 161 PheGluGluProThrSerSerLeuAlaGlnIleLeuAlaSerValSerValValPhe 180  
 Db 907 TTCGAGGAGCCACGCTGCTGCTGCGCGCGAGATCTTGGTAGCGTGTGCTGCTGTC 966  
 Qy 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200  
 Db 967 GTGATCGTGTCCATGGTGTGTGTGCGCGACACGTTGCGCGACTGCGCGCAACGAC 1026  
 Qy 201 AlaAspAsnArgSerLeuAspArgSerArg----- 211  
 Db 1027 GCGCAACCGGAGCTGTGATACCGGAGCGAGTACTCGCGGCGCTCGGAGGAGCGCC 1086  
 Qy 212 -----IleIleGluAlaIleCysIleGlyTyrPheThrAlaGluCysIleValArgPhe 229  
 Db 1087 TCCGGGATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCTGCTGAGGTT 1146  
 Qy 230 IleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeu 249  
 Db 1147 ATTGTCTCCAAACAAAGTGTAGTTGTTCAGAGAGACCCCTGAACATCATGATTACTG 1206  
 Qy 250 AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln 269  
 Db 1207 GCAATCAGCGGTATTCATCTCTGTGTGTGATGACAGTGTTCAGCGCGAGACTCTCA 1266  
 Qy 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle 289  
 Db 1267 CTCAGAGCGCTGAGTCACTTGAGGTACTTAGAATGATCAGGATTTTGGGTGATT 1326  
 Qy 290 LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr 309  
 Db 1327 AAGCTTGCCCGTCACTTCATTGGTCTTCAGACACTCGGTTTGACTCTCAACAGTGTCTAC 1386  
 Qy 310 ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu 329  
 Db 1387 CGAGAGATGGTTATGTACTTCTTCTTCTTGTGTTGCTGCTGCAATCTTTAGTGCACT 1446  
 Qy 330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349  
 Db 1447 TCTAGCTTCTTGAACATGGCTGACCTGGAACATCCACACAGGATTTTACCAGCAT 1506  
 Qy 350 ProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyr 369  
 Db 1507 CTTGCTGCTGCTGCTGGTGGTGGTATTCATATGATCAGTGTGCTATGGAGATATGAT 1566  
 Qy 370 ProfileThrProGlyArgIleLeuGlyValCysValValSerGlyIleValLeu 389  
 Db 1567 CCTATCACAGTCCCTGGAAGATTTCTGAGGAGTTTGTGTGTGTGTCAGTGAATTTGTTCTA 1626

Qy 390 LeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409  
 Db 1627 TTGGCAATACCTATCACTTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGCTCAAG 1686  
 Qy 410 PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425  
 Db 1687 TTTAGATCTCTAGTATAGTAGAGCTCTCCACTGAAATTCCTGAT 1734  
 RESULT 7  
 PCT-US03-28227-1172  
 ; Sequence 1172, Application PC/TUS0328227  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;  
 ; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;  
 ; APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;  
 ; APPLICANT: HARTSHORNE, Toinette A.; SUCHOROLSKI, Martin;  
 ; APPLICANT: ELDER, Christina M.; PITTS, Steven J.;  
 ; APPLICANT: ALDER, Linda V.; MOONEY, Elizabeth M.;  
 ; APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;  
 ; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;  
 ; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;  
 ; APPLICANT: PANZER, Scott R.; WANG, Xinhao;  
 ; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;  
 ; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;  
 ; APPLICANT: RIAUX, Pierre; SHEN, Edward J.;  
 ; APPLICANT: WU, Mingham C.; STUVE, Laura L.;  
 ; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;  
 ; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;  
 ; APPLICANT: VITT, Ursula A.; KIRTON, Edward;  
 ; APPLICANT: XU, Yuming; KWONG, Mary;  
 ; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;  
 ; APPLICANT: MA, Yan; JACKSON, Jennifer L.;  
 ; APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;  
 ; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.  
 ; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: PN-0100 PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US03/28227  
 ; CURRENT FILING DATE: 2003-09-12  
 ; PRIOR APPLICATION NUMBER: US 60/410,260  
 ; PRIOR FILING DATE: 2002-09-12  
 ; PRIOR APPLICATION NUMBER: US 60/410,259  
 ; PRIOR FILING DATE: 2002-09-12  
 ; NUMBER OF SEQ ID NOS: 5444  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1172  
 ; LENGTH: 2405  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No: 937585.PT34  
 PCT-US03-28227-1172  
 Alignment Scores:  
 Pred. No.: 1,94e-207 Length: 2405  
 Score: 2106.00 Matches: 407  
 Percent Similarity: 98.31% Conservative: 0  
 Best Local Similarity: 98.31% Mismatches: 1  
 Query Match: 95.08% Indels: 7  
 DB: 1 Gaps: 1  
 US-10-016-647-2 (1-425) x PCT-US03-28227-1172 (1-2405)  
 Qy 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20  
 Db 597 ATGACCTTCGGCGCAGCGGCGGCTCGGTGGTGTGTAACGTGGCGCGCGCGGTAT 656  
 Qy 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40  
 Db 657 TCCTGTGCCGGAGCTGCTGAAGGACTTCCCTCGCGCGCTGAGCGCGCGTGCACGCG 716  
 Qy 41 CysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGlu 60

717	Db	TGCGGCTCCGAGCGCGACGTGCTCGAGGTGCGACGACTACGACCGCGAGCGCAACGAG	776
61	Qy	TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis	80
777	Db	TACTTCTTCGACCGGCACCTCGAGGCGCTTCGGCTTTCATCTCTACGTGCGCGCCAC	836
81	Qy	GlyIysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr	100
837	Db	GGCAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTTCCTTCTACACGAGATGATCTAC	896
101	Qy	TrpGlyLeuGluAlaHisLeuGluTyrCysGlnArgArgLeuAspAspArgMet	120
897	Db	TGGGGCTTCGAGGGCGCGACCTCGAGTACTGCTGCCAGCGCCCTCGACGACGCGATG	956
121	Qy	SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValIleuGlyArgAspGluAla	140
957	Db	TCCGACACCTACACCTTCTACTCGCGCGACGACCGGGCGTGTGGGCGCGACGAGGCG	1016
141	Qy	ArgProGlyAlaGluAlaAlaProSerArgArgTrrpLeuGluArgMetArgArgThr	160
1017	Db	CGCCCGCGGGCGCGAGGGCTCCCTCCAGGGCTGGCTGGAGCGCATGCGCGCGACC	1076
161	Qy	PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPhe	180
1077	Db	TTGAGGAGGCCCAATC-----CTGCGCTAGCGTGTGCGTGGTGTTC	1117
181	Qy	ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrrpArgAsnAlaAla	200
1118	Db	GTGATCGTGCCATGGTGGTGTGTGGCGCAGACAGTGTGCCGACTGGCGCAACGCGACC	1177
201	Qy	AlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTrrp	220
1178	Db	GCCGACAAACCGAGCCTGGATGACCGCGAGCAGGATATTTCGAAGCTATCTGCATAGTTGG	1237
221	Qy	PheThrAlaGluCysIleValArgPheIleValSerIysAsnIysCysGluPheValLys	240
1238	Db	TTCACTGCCGAGTGCACTCGTAGGTTCAATTGTCTCCAAAACAAAGTGTAGTTGTCAAG	1397
241	Qy	ArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTrrIleSerValLeuMet	260
1298	Db	AGACCCCTGAACATCATTTACTGGCAATCAGCCGATTTACATCTCTGTGTTCATG	1357
261	Qy	ThrValPheThrGlyGluAsnSerGlnLeuGluArgAlaGlyValThrLeuArgValLeu	280
1358	Db	ACAGTGTTTACAGCGGAACTCTCAACTCCAGAGGCGTCGAGTCACTTTGAGGGTACTT	1417
281	Qy	ArgMetMetArgIlePheTrrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr	300
1418	Db	AGAATGATGAGGATTTTTTGGGTGATTAACTTGGCCGTCACCTTGTCTTCAGACA	1477
301	Qy	LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys	320
1478	Db	CTCGGTTTGACTCTCAAACTTGCTACCGAGAGATGGTTATGTATTCTTGTCTTCAATTGT	1537
321	Qy	ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu	340
1538	Db	GTTGCCATGGCAATCTTTAGTGCACTTCTTCAGCTTTCGCCGTCACCTTGTCTTCAGAA	1597
341	Qy	ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrrpValIleIleSerMet	360
1598	Db	ACATCCAAACAGGACTTTACCAGCAATTCCTGCTGCTGCTGGTGGGTGATTACTCTATG	1657
361	Qy	ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly	380
1658	Db	ACTACAGTTCGGCTATGGAGATATGATPCTTATCACAGTGCCTCGAAGAAATCTTGAGGA	1717
381	Qy	ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer	400
1718	Db	GTTTGTGTTGTCAGTGGAAATGTTCTATTTCGCATTACCTATCACTTTTATCTACCATAGC	1777
401	Qy	PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArg	414
1778	Db	TTTGTGCAGTGTATCATGACTCATGCTCAAGTTTAGATCTGCTAGG	1819

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RESULT 8
PCT-US02-10780-45
, Sequence 45, Application PC/TUS0210780
, GENERAL INFORMATION:
, APPLICANT: Curagen Corporation
, APPLICANT: Guo, Xiaojia
, APPLICANT: Kekuda, Ramesh
, APPLICANT: Miller, Charles E.
, APPLICANT: Malyanekar, Uriel M.
, APPLICANT: Spytek, Kimberly A.
, APPLICANT: Patturajan, Meera
, APPLICANT: Liu, Ziaohong
, APPLICANT: Gusev, Vladimir Y.
, APPLICANT: Li, Li
, APPLICANT: Vernet, Corine
, APPLICANT: Zerhusen, Bryan D.
, APPLICANT: Gorman, Linda
, APPLICANT: Shenoey, Suresh G.
, APPLICANT: Pena, Carol E.A.
, APPLICANT: Smithson, Glenda
, APPLICANT: Burgess, Catherine E.
, APPLICANT: Gerlach, Valerie
, APPLICANT: Padigaru, Muralidhara
, APPLICANT: Shimkets, Richard A.
, APPLICANT: Gangolli, Esha A.
, APPLICANT: Taupier Jr., Raymond J.
, APPLICANT: Casman, Stacie J.
, APPLICANT: Ji, Weishen
, APPLICANT: Anderson, David W.
, APPLICANT: Liete, Mario W.
, APPLICANT: Rastelli, Luca
, APPLICANT: Edinger, Shlomit R.
, APPLICANT: Stone, David J.
, APPLICANT: MacDougall, John R.
, APPLICANT: Rothenberg, Mark E.
, TITLE OF INVENTION: Novel Proteins an
, FILE REFERENCE: 21402-322C-061
, CURRENT APPLICATION NUMBER: PCT/US02/
, CURRENT FILING DATE: 2002-04-03
, PRIOR APPLICATION NUMBER: 10/114,270
, PRIOR FILING DATE: 2002-04-02
, PRIOR APPLICATION NUMBER: 60/281,086
, PRIOR FILING DATE: 2001-04-03
, PRIOR APPLICATION NUMBER: 60/281,136
, PRIOR FILING DATE: 2001-04-03
, PRIOR APPLICATION NUMBER: 60/281,863
, PRIOR FILING DATE: 2001-04-05
, PRIOR APPLICATION NUMBER: 60/281,906
, PRIOR FILING DATE: 2001-04-05
, PRIOR APPLICATION NUMBER: 60/282,020
, PRIOR FILING DATE: 2001-04-06
, PRIOR APPLICATION NUMBER: 60/282,930
, PRIOR FILING DATE: 2001-04-10
, PRIOR APPLICATION NUMBER: 60/282,934
, PRIOR FILING DATE: 2001-04-10
, PRIOR APPLICATION NUMBER: 60/283,512
, PRIOR FILING DATE: 2001-04-12
, PRIOR APPLICATION NUMBER: 60/283,710
, PRIOR FILING DATE: 2001-04-13
, Remaining Prior Application data remo
, NUMBER OF SEQ ID NOS: 470
, SEQ ID NO 45
, LENGTH: 1651
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: CDS
, LOCATION: (1)..(1642)
PCT-US02-10780-45

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Alignment Scores:	
Pred. No.:	1.46e-206
Length:	1651

Score: 2095.50 Matches: 411  
Percent Similarity: 91.54% Conservative: 0  
Best Local Similarity: 91.54% Mismatches: 3  
Query Match: 94.60% Indels: 35  
DB: 1 Gaps: 3

US-10-016-647-2 (1-425) x PCT-US02-10780-45 (1-1651)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20  
Db 58 ATGACCTTCGGCGCGAGCGGGCGGCTCGGTGGTCTGAACGTGGCGGCGCGCGGTAT 117  
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40  
Db 118 TCGCTGTCGGCGAGCTGCTGAAGACTTCCTCCGCTGCGCGCGGTGAGCGCGGTGACCGC 177  
QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60  
Db 178 TCCCGCTCCGAGCGGACGCTGCTCGAGGTGTCGACGACTACGACCGCGAGCGCAACGAG 237  
QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80  
Db 238 TACTTCTCGACCGGCACTCGAGGCTTCGGCTTCATCTCTAGTGGCGGCGCAC 297  
QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100  
Db 298 GGCAGAGCTCGCTTCGGCGCGGATGTGCGAGCTCTCTCTACACGAGATGATCTAC 357  
QY 101 TrpGlyLeuGluGlyValAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAspArgMet 120  
Db 358 TGGGCGCTGGAGGCGCGGCACTCGAGTACTGCTCCAGCGCGGCTCGACACCGCATG 417  
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140  
Db 418 TCCGACACCTACACTTCTACTCGCGCGAGCGCGGCGTCTGGCGCGCGAGCGC 477  
QY 141 ArgProGly-----GlyAlaGluAlaPro--- 149  
Db 478 CGCCCCGGCGCGAGCGGCTCCCTCCAGCGCGTGGTGGAGCGCATGGCGCGACCTT 537  
QY 150 -----SerArgArgTyrLeuGluArgMetArgArgThrPhe 161  
Db 538 CGAGGAGCCCGCTCGTGGCGCGAGCGCTGCTGGAGCGCATGGCGCGGACCTTC 597  
QY 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheVal 181  
Db 598 GAGGAGCCACGCTCGTGGTGGCGCGAGATCTCGGTAGCGTGTGGTGTGTGTGTGTGT 657  
QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAlaAla 201  
Db 658 ATCGTGTCCATGGT 717  
QY 202 AspAsnArgSerLeuAspAspArgSer----- 210  
Db 718 GACAAACCGAGCGCTGGATACCGGAGCAGGTACTCCGCGGCGCTGGAGGAGCGCTCC 777  
QY 211 -----ArgIleGluAlaIleCysIleGlyTyrPheThrAlaGluCys 225  
Db 778 GGGTGTCTCTTCAGGAGGATAATTGAAGTACTGCATAGGTGTGTGTGTGTGTGTGTGTGT 837  
QY 226 IleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIle 245  
Db 838 ATCGTGAGGTTTCACTGTCTCCAAACAAAGTGTGAGTTGTCAAGAGACCCCTGACATC 897  
QY 246 IleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGly 265  
Db 898 ATTGATTTACTGGCAATCACGCGGATTACATCTCTGTGTGTGTGTGTGTGTGTGTGTGT 957  
QY 266 GluAsnSerGlnLeuGluArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle 285  
Db 958 GAGAACTCTCACTCCAGAGGCGTGGAGTCCACTTGGAGGTACTTAGAATGATGAGGATT 1017  
QY 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeu 305

Db 1018 TTTTGGGTGATTAAAGCTTGGCCGTCATTTCATTTGGTCTTCAGACACTCGGTTGACTCTC 1077  
QY 306 LysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIle 325  
Db 1078 AAACGTTGCTACCGAGAGATGGTATTGTTACTTGTCTTCTTCTTGTGTGTGTGTGTGTGT 1137  
QY 326 PheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345  
Db 1138 TTTAGTGCACCTTTCTCAGCTTCTTGAACATGGGTGGACCTGGAAACATCCAACAGGAC 1197  
QY 346 PheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyr 365  
Db 1198 TTTTACCAGCATTCCTGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTTGGCTAT 1257  
QY 366 GlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSer 385  
Db 1258 GGAGATATGATCTCTATCACAGTCCCTGGAGAAATCTTGGAGGAGTTTGTGTGTGTGT 1317  
QY 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405  
Db 1318 GGATTCGTTCTATTGGCATTCACCTATCATTCTTATCTACCATAGCTTTGTGCAGTGTAT 1377  
QY 406 HisGluLeuLysPheArgSerAlaArg 414  
Db 1378 CATGAGCTCAAGTTTAGATCTGCTAGG 1404

RESULT 9  
US-10-114-270-45  
; Sequence 45, Application US/10114270  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Liu, Zhaozhong  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Li, Li  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Gangolli, Esna A.  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Anderson, David W.  
; APPLICANT: Liote, Mario W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Stone, David J.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Rothenberg, Mark E.  
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-322C  
; CURRENT APPLICATION NUMBER: US/10/114,270  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/281,086  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05







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; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,561
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7482060CB1
US-10-415-378-39

Alignment Scores:
Pred. No.: 2,056-204 Length: 2235
Score: 2076.50 Matches: 406
Percent Similarity: 97.83% Conservative: 0
Best Local Similarity: 97.83% Mismatches: 1
Query Match: 93.75% Indels: 9
DB: 51 Gaps: 2

US-10-016-647-2 (1-425) x US-10-415-378-39 (1-2235)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
Db 428 ATGACCTTCGGCGGAGCGGGCGGCTCGGTGGTGGTGAACGTGGGGCGGCCGGGTAT 487
QY 21 SerLeuSerArgGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 488 TGGCTGTCCGGAGGAGCTGTGAAGGACTTCCCGCTGCGCGCGGTGAGCGCGGTGACCGCG 547
QY 41 CysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGlu 60
Db 548 TGGCGCTCCGAGCGGACGCTGCTCGAGGTGTGCGAGCACTACGACCGCGAGCGCAACGAG 607
QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80
Db 608 TACTTCTTCGACCGGCACCTCGGAGGCGCTTCGGCTTCATCTCTCTACGTGGCGGCGCAC 667
QY 81 GlyLeuLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 668 GGCAGCTCGCTTCGGCGCGGAGATGTGCGAGCTCTCTCTTACACGAGATGATCTAC 727
QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
Db 728 TGGGCGCTGGAGGGCGGCGCACCTCGAGTACTGCTGCCAGCGCGGCTCGACGCGCATG 787
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 788 TCGACACCTACACCTTCTACTTCGCGCCGACGAGCGGCGGTCTGGCGCGGAGCGGCG 847
QY 141 ArgProGlyGlyAla-GluAlaAlaProSerArgArgTrpLeuGluArgMetArgGlyHis 160
Db 848 CGCCCC---GGCGCGGAGGCGGCTCCCTCCAGGCGCTGGCTGGAGCGCATGCGGCGGAC 904
QY 160 rPheGluGluProThrSerSerLeuAlaAlaClnleuAlaSerValSerValValph 180
Db 905 CTTGAGGAGGCCACATC-----CTGGCTAGCGGTGCGGTGGTGT 945

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QY 180 eValileValSerMetMetValValLeuCysAlaSerThrLeuProSerThrArgAsnAlaAl 200
Db 946 CGTGATCGTGTCCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1005
QY 200 aAlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTr 220
Db 1006 CGCCGACAAACCGCAGCTGGATGACCGGAGGAGGATATTTGAAGCTATCTGCATAGGTTG 1085
QY 220 pPheThrAlaGluCysIleValaIleGlyPheIleValSerIleAsnLysCysGluPheVal 240
Db 1066 GTTCACTGCCAGTGCATCGTGAGGTGATTTGTCTCCAAAAACAAGTGTGAGTTGTCAA 1125
QY 240 sArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMe 260
Db 1126 GAGACCCCTGAACATCATTTACTGGCAATCAGCCGATTTACATCTCTGTGTGTAT 1185
QY 260 tThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLe 280
Db 1186 GACAGTGTTTACAGCGGAGAACTCTCAACTCCACAGGCGTGGAGTCACTTGGAGGTACT 1245
QY 280 uArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnTh 300
Db 1246 TAGAATGATGAGGATTTTGGGTGATTAAGCTTGGCGGTCACTTCACTTGTCTTCAGAC 1305
QY 300 rLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCy 320
Db 1306 ACTCGGTTTGACTCTCAACGCTTGTACCGAGAGATGGTATGTATTCTTCTTCAATTG 1365
QY 320 sValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGl 340
Db 1366 TGTGGCCATGGCAATCTTTAGTGACATTTCTCAGCTTCTTGAACATGGGTGGACCTGGA 1425
QY 340 uThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMe 360
Db 1426 AACATCCAAACAGGACTTACCAGATTCCTGCTGCTGCTGGTGGGTGATTATCTCTAT 1485
QY 360 tThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGl 380
Db 1486 GACTACAGTTGGCTATGGAGATATGTATCTATCACAGTGCCTGGAAGATTTCTTGGAGG 1545
QY 380 yValCysValValSerGlyIleValLeuLeuLeuAlaLeuProIleThrPheIleTyrHisSe 400
Db 1546 AGTTTGTGTGTGAGTGAATTTGTTATTGGCAATACCTATCATTCTTATCTACCATAG 1605
QY 400 rPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArg 414
Db 1606 CTTTGTGCAGTGTATCATGAGCTCAAGTTAGATCTGCTAGG 1648

RESULT 11
US-10-343-903-47
; Sequence 47, Application US/10343903
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry;
; APPLICANT: THORNTON, Michael; RAMKUMAR, Jayalaxmi;
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; YANG, Junming;
; APPLICANT: YAO, Monique G.; LAL, Preeti G.;
; APPLICANT: CHAWLA, Narinder K.; GANDHI, Ameena R.;
; APPLICANT: HAPALIA, April J.A.; NGUYEN, Danielle B.;
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: TRIBOULEY, Catherine M.; LU, Dyung Aina M.;
; APPLICANT: XU, Yuming; REDDY, Roopa;
; APPLICANT: HERNANDEZ, Roberto; BOROWSKY, Mark L.;
; APPLICANT: LO, Terence P.; LU, Yan;
; APPLICANT: POLICKY, Jennifer L.; GREENE, Barrie D.;
; APPLICANT: SANJANWALA, Madhusudan M.; RAUMANN, Brigette E.;
; APPLICANT: BURFORD, Neil; ISON, Craig H.;
; APPLICANT: LEE, Brnestine A.; DING, Li;
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.;
; APPLICANT: KEAN, Farrah A.; SEILHAMER, Jeffrey J.;
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0183 USN
; CURRENT APPLICATION NUMBER: US/10/343,903

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; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: PCT/US01/24217
; FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/231,434
; FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/230,067
; FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/228,140
; FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/226,410
; FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/224,456
; FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/223,269
; FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PERL Program
; SEQ ID NO 47
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474111CB1
US-10-343-903-47

Alignment Scores:
Pred. No.: 2,696-171 Length: 2312
Score: 1758.00 Matches: 351
Percent Similarity: 83.37% Conservative: 0
Best Local Similarity: 83.37% Mismatches: 0
Query Match: 79.37% Indels: 70
DB: 49 Gaps: 1

US-10-016-647-2 (1-425) x US-10-343-903-47 (1-2312)
Qy 5 ArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArg 24
Db 790 CGAGCGGGCGCGCTCGTGGTGTGCTGAACGTGGCGGGCGCGCTGATTCGCTGTCGGG 849
Qy 25 GluLeuLeuValAspPheProLeuArgArgValSerArgLeuHisGlyCysArgSerGlu 44
Db 850 GAGCTGCTGAAGACTTCCCGCTGCGCGGTGAGCGGGCTGACCGCTGCGCTCCGAG 909
Qy 45 ArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGluTyrPhePheAsp 64
Db 910 CGCGACGTGCTCGAGGTGTGCGACGACTACGACCGCGAGCGCAACGAGTACTTCTTCGAC 969
Qy 65 ArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArg 84
Db 970 CGGCACGCGAGGCTTCGCGCTTCATCTCTCTAC----- 1005
Qy 85 PheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGlu 104
Db 1005 ----- 1005
Qy 105 GlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAspArgMetSerAspThrTyr 124
Db 1005 ----- 1005
Qy 125 ThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGlyGly 144
Db 1005 ----- 1005
Qy 145 AlaGluAlaProSerArgArgTyrTrpLeuArgValArgMetArgThrPheGluGluPro 164
Db 1006 -----CGCGCTCCCTCCAGCGCTGCGTGGAGCGCATGCGCGGACCTTCGAGGAGCCC 1059
Qy 165 ThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSer 184
Db 1060 ACGTCGTCGTCGCGCGGCGAGATCTCGCTAGCGGTGTCGCTGCTGCTGTCGTCGTCGTC 1119
Qy 185 MetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAspAsnArg 204
Db -----

; US-10-170-235-1828
; Sequence 1828, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 1828
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-1828

Alignment Scores:
Pred. No.: 8e-169 Length: 1416
Score: 1731.50 Matches: 340
Percent Similarity: 91.05% Conservative: 6
Best Local Similarity: 89.47% Mismatches: 5



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QY 289 IleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCys 308
Db 592 ATCAAGCTTGGCCGACCTTCATTGGTCTGCAGACACTGGGCTTGACTCTCAAGCGGTGC 651
QY 309 TyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAla 328
Db 652 TACCGAGAGATGCTATGTTACTTGTCTTCACTGTGTGTTGCCATGCACTTTTAGTGCA 711
QY 329 LeuSerGluLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSer 348
Db 712 CTCTCTCAGTCTCTTGAACATGGGCTGGACCTTGGAAACATCCACACAGGATTTCCCCAGC 771
QY 349 IleProAlaAlaCysTrpTrpValIleSerMetThrThrValGlyTyrGlyAspMet 368
Db 772 ATCCCCGCTGCCTGCTGGTGGTGAATATCTCTATGACTACAGTTGGCTATGGAGATATG 831
QY 369 TyrProIleThrValProGlyArgIleLeuGlyValCysValValSerClyIleVal 388
Db 832 TATCTTATCAGGTGCTCGAAGAAATCTTGGAGGAGTTTGTGTGAGTGGGATTTGT 891
QY 389 LeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu 408
Db 892 CTGTGGCATTAACCATCACTTTCATCTACCATAGCTTTGTGCAGTGTCTACCCAGAGCTC 951
QY 409 LysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
Db 952 AAGTTTAGATCGCTAGATATAGTAGGAGCCTCTCAGCTGAGTTCTCTGAAT 1002

RESULT 14
US-60-360-207-10588
; Sequence 10588, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360,207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 10588
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-10588

Alignment Scores:
Pred. No.: 2,89e-162 Length: 1005
Score: 1666.50 Matches: 322
Percent Similarity: 97.03% Conservativity: 5
Best Local Similarity: 95.55% Mismatches: 7
Query Match: 75.24% Indels: 3
DB: 93 Gaps: 1

US-10-016-647-2 (1-425) x US-60-360-207-10588 (1-1005)

QY 89 MetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeu 108
Db 1 ATGTGGAGCTCTCTTCTTCAACAGAGATGATCTACTGGGGCTTGGAGGTGGCCACCTG 60
QY 109 GluTyrCysGlnArgLeuAspArgMetSerAspThrTyrThrPheTyrSer 128
Db 61 GAGTACTGTGTCAGCGCGCTAGACCGCATGTCGACACCCACACCTTTTCCACCGG 120
QY 129 AlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyValAlaGluAla 148
Db 121 GCAGACGAG-----CTGGGCGCGAGACGCTCGTCCCGCGGACCGCGGCGGCC 171
QY 149 ProSerArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeu 168
Db 172 CCTTCCGCGCTGGCTGGAGCGCATGCGCGGACCTTTCGAGAGCCACCGTCGTCGTG 231
QY 169 AlaAlaGluIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188

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Db 232 GCCCGCAGATCTCGCCAGCGGTGTCGGTGGTGTTCGTGATCGTGTCCATGGTGGTGCTG 291
QY 189 CysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArgSerLeuAspAsp 208
Db 292 TGGCCAGACAGCTGCGGACTGCGGTGGCGCGGTGCTGACAAACCGCAGTCTGGATGAC 351
QY 209 ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArg 228
Db 352 CGGAGCAGGATAATTGAAGCTATCTGCATAGGTGGTTTCCCGCGAGTGCACTGTCGCG 411
QY 229 PheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeu 248
Db 412 TTATCTGCTTCCAAAACAACTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGACTTA 471
QY 249 LeuAlaIleThrProTyrTrpIleSerValLeuMetThrValPheThrGlyGluAsnSer 268
Db 472 CTGGCAATCAACGCCCTATTACATCTCTGTGCTAATGACAGTGTTCACAGCGCAGAACTCT 531
QY 269 GluLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTyrVal 288
Db 532 CAACTCCAGAGGGCTGGGGTCACTTGGAGGTCTCCGAATGATGGGATCTTCTGGGTG 591
QY 289 IleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCys 308
Db 592 ATCAAGCTTCCCGGCACCTTCATTGGTCTGCAGACACTGGGCTTGACTCTCAAGCGGTGC 651
QY 309 TyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAla 328
Db 652 TACCGAGAGATGTCATGTTACTTGTCTTCTATCTGTGTGGCATGCACTTTTAGTGCA 711
QY 329 LeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSer 348
Db 712 CTCTCTCAGTCTCTTGAACATGGGCTGGACCTGGAAACATCCACCAAGGATTTGCCAGC 771
QY 349 IleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMet 368
Db 772 ATCCCCGCTGCCTGCTGGTGGTGAATATCTCTATGACTACAGTTGGCTATGGAGATATG 831
QY 369 TyrProIleThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleVal 388
Db 832 TATCTTATCAGGTGCTCGAAGAAATCTTGGAGGAGTTTGTGTGTCAGTGGGATTTGT 891
QY 389 LeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu 408
Db 892 CTGTGGCATTAACCATCACTTTCATCTACCATAGCTTTGTGCAGTGTCTACCCAGAGCTC 951
QY 409 LysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
Db 952 AAGTTTAGATCGCTAGATATAGTAGGAGCCTCTCAGCTGAGTTCTCTGAAT 1002

RESULT 15
US-60-196-712-1268
; Sequence 1268, Application US/60196712
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000451
; CURRENT APPLICATION NUMBER: US/60/196,712
; CURRENT FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 3846
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1268
; LENGTH: 695
; TYPE: DNA
; ORGANISM: HUMAN
US-60-196-712-1268

Alignment Scores:
Pred. No.: 5.24e-105 Length: 695
Score: 1113.50 Matches: 218
Percent Similarity: 98.64% Conservativity: 0

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Best Local Similarity: 98.64% Mismatches: 0  
Query Match: 50.27% Indels: 3  
DB: 75 Gaps: 1

US-10-016-647-2 (1-425) x US-60-196-712-1268 (1-695)

QY 205 SerLeuAspArgSerArgIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224  
DB 9 TCCTTTGAC-----AGGATAATTGAAGCTATCTGCATAGTTGGTTCACCTGCCGAG 59

QY 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244  
DB 60 TGCATCGTGAGGTTCTCTCCAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAC 119

QY 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264  
DB 120 ATCATTTAATTACTGGCAATCAGCCGTATTACATCTCTGTGTGATGACAGTGTTTACA 179

QY 265 GlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArg 284  
DB 180 GCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACCTTCAGGGTACTTAGAATGATGAGG 239

QY 285 IlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThr 304  
DB 240 ATTTTGGGTGATTAAAGCTTGCCCGTACTTCATTGGTCTTCAGACACTCGGTTTGACT 299

QY 305 LeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAla 324  
DB 300 CTCAAACGTTGTACCGAGAGATGTTATGTACTTGTCTTATTGTGTGCCATGGCA 359

QY 325 IlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLys 344  
DB 360 ATCTTTAGTGCACCTTCTCAGCTTCTTGAAACATGGGCTGGACCTGGAAACATCCCAACAG 419

QY 345 AspPheThrSerIleProAlaAlaCysTrpTyrValIleIleSerMetThrThrValGly 364  
DB 420 GACTTTACCAGCATTCCTGCTGCTGCTGGTGGTGATTATCTCTATGACTACAGTTGGC 479

QY 365 TyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGlyValCysValVal 384  
DB 480 TATGGAGATATGTATCTATCACAGTGCCTGGAAGAAATTCCTGGAGGAGTTTGTGTGTC 539

QY 385 SerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCys 404  
DB 540 AGTGGAAATTGTCTATGTGCATATACCTATCATCTTTATCTACCATAGCTTTGTGCAGTGT 599

QY 405 TyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeu 424  
DB 600 TATCATGAGCTCAAGTTTAGACTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTG 659

QY 425 Asn 425  
DB 660 AAT 662

Search completed: April 19, 2004, 16:44:38  
Job time : 4387 secs

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Db      62  CTGAGGCGCATCGCGGACCTTCGAGGAGCCACGTCGTCGTCGCGCGGAGATCCTG 121
Qy      174  AlaserValSerValValPheValIleValSerMetValValLeuValLeuValSerThrLeu 193
Db      122  GCTAGCGTGTGCGTGTGTTGTCGTATCGTGTCCATGCTGTGTGCGCCAGCAGTTG 181
Qy      194  ProAspTTPArgAsnAlaAlaAlaAspAsnArgSerLeuAspArgSerArgIleIle 213
Db      182  CCCGACTGGCGCAACGAGCGCGGCAACCGGAGCTGTGATACCGGAGGAGGATAAT 241
Qy      214  GluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerIys 233
Db      242  GAAGCTATCTGCATAGTTGTTCACTGCGGAGTGCATCGTAGGTTTCATTGTCCTCAA 301
Qy      234  AsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrPro 253
Db      302  AACAGTGTGAGTTGTCAAGAGACCCCTGAACATCATTTATGTCGAATCAGCGG 361
Qy      254  TyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnAla 273
Db      362  TATTACATCTCTGTGTGATGACAGTGTTCACAGGCGAGAACTCTCAACTCCAGAGGCT 421
Qy      274  GlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArg 293
Db      422  GGAGTCACCTTGAGG----- 436
Qy      294  HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetVal 313
Db      437  -----ACACTCGGTTTGACTCTCAACGTTGCTACCGAGAGATGTT 478
Qy      314  MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
Db      479  ATGTTACTTGTCTTCACTTTGTTGTCATGCGCAATCTTTAGTGACATTTCTCAGCTTCT 538
Qy      334  GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db      539  GAACATGGCTGGACCTGGAACATCCAAAGGAGCTTTACCAGCATTCCTGCTGCCTGC 598

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RESULT 4
US-60-545-213-8467
; Sequence 8467, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8467
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-8467

Alignment Scores:
Pred. No.: 1,28e-111 Length: 600
Score: 983.50 Matches: 199
Percent Similarity: 90.45% Conservative: 0
Best Local Similarity: 90.45% Mismatches: 0
Query Match: 44.40% Indels: 21
DB: 7 Gaps: 1

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US-10-016-647-2 (1-425) x US-60-545-213-8467 (1-600)
Qy      134  ValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgTrp 153
Db      2  GTGCTGGGCGCGAGCGAGCGGCGCGCGCGGCGGCGGCGGCTCCCTCCAGGCGCTGG 61
Qy      154  LeuGluArgMetArgTrpPheGluGluProThrSerSerLeuAlaAlaGlnIleLeu 173

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Db      62  CTGAGGCGCATCGCGGACCTTCGAGGAGCCACGTCGTCGTCGTCGCGCGGAGATCCTG 121
Qy      174  AlaserValSerValValPheValIleValSerMetValValLeuValLeuValSerThrLeu 193
Db      122  GCTAGCGTGTGCGTGTGTTGTCGTATCGTGTCCATGCTGTGTGCGCCAGCAGTTG 181
Qy      194  ProAspTTPArgAsnAlaAlaAlaAspAsnArgSerLeuAspArgSerArgIleIle 213
Db      182  CCCGACTGGCGCAACGAGCGCGGCAACCGGAGCTGTGATACCGGAGGAGGATAAT 241
Qy      214  GluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerIys 233
Db      242  GAAGCTATCTGCATAGTTGTTCACTGCGGAGTGCATCGTAGGTTTCATTGTCCTCAA 301
Qy      234  AsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrPro 253
Db      302  AACAGTGTGAGTTGTCAAGAGACCCCTGAACATCATTTATGTCGAATCAGCGG 361
Qy      254  TyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnAla 273
Db      362  TATTACATCTCTGTGTGATGACAGTGTTCACAGGCGAGAACTCTCAACTCCAGAGGCT 421
Qy      274  GlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArg 293
Db      422  GGAGTCACCTTGAGG----- 436
Qy      294  HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetVal 313
Db      437  -----ACACTCGGTTTGACTCTCAACGTTGCTACCGAGAGATGTT 478
Qy      314  MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
Db      479  ATGTTACTTGTCTTCACTTTGTTGTCATGCGCAATCTTTAGTGACATTTCTCAGCTTCT 538
Qy      334  GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db      539  GAACATGGCTGGACCTGGAACATCCAAAGGAGCTTTACCAGCATTCCTGCTGCCTGC 598

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RESULT 5
US-10-796-280-586
; Sequence 586, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 586
; LENGTH: 4656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-586

Alignment Scores:
Pred. No.: 2,35e-84 Length: 4656
Score: 774.50 Matches: 171
Percent Similarity: 59.53% Conservative: 82
Best Local Similarity: 40.24% Mismatches: 162
Query Match: 34.97% Indels: 12
DB: 6 Gaps: 5

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US-10-016-647-2 (1-425) x US-10-796-280-586 (1-4656)
Qy      1  MetThrPheGlyArgSerGlyAlaAlaser-----ValValLeuAsnValGlyAla 18
Db      225  ATGAGATGTGCGCAGCAAGGCGTCTCTCGCGGCGTCCGCTCAACGTCGGGGGCTG 284
Qy      19  ArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeu 38
Db      285  GCGCAGCAGGAGTACTCTGCGCTACCTTGACCGCTGCGCGCGCTGCGCGCTGCGCAAGCTC 344

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39 HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58  
345 CGGACTGCAACACGAGCAGCTCGCTCGAGGTGCGGATGACTACGACCTCGACGAC 404  
59 AsnGluTyr-PhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArg 78  
405 AACGAGTACTTCTTTCACCGCACCCGGCGCCTTCACCTCCATCTCAACTTCTACCGC 464  
79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98  
465 ---ACTGGGCGACTGCACATGATGGAGGAGATGTGGCGCTAGCTTCAGCCCAAGAGCTC 521  
99 IleTyrTrpGlyLeuGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAsp 118  
522 GACTACTGGGGCATCGACGAGATCTACTTGGAGTCTGCTGCCAGGCGCTACCAACCAG 581  
119 ArgMetSerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAsp 138  
582 AAGAAAGAGCAGATGA--ACGAGGAGCTCAAGCGTGAGCGCCGAGACYCTACGGGACGGG 639  
139 GluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArg 158  
640 AAGCGAGGAGTTCGATAACACGTGTGCGCA--GAGAAGAGG-----AAAAAAGCTCGG 692  
159 ArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerVal 178  
693 GACCTACTGGAGAAGCCAAATTCCTGTGTGGCTGCCAAGATCTCTGCCATAATTTCCATC 752  
179 ValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsn 198  
753 ATGTTTCATGCTCTCTCCACATGCGCTCTCCCTCAACACGCTGCTGAGCTACAGAGC 812  
199 AlaAlaAlaAspAsnArgSerLeuAspAsp---ArgSerArgIleIleGluAlaIleCys 217  
813 CTCGATGAGTTGGCCAGTCCACAGACAACCCCGAGCTGGCCCCACGTGGAGGCGGTGTGC 872  
218 IleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGlu 237  
873 ATCGCATGGTTCACCATGGAGTAGTACCTGCTGAGGTTCCTCTCTCGCCCAAGAAGTGGAG 932  
238 PheValLysArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSer 257  
933 TTCTTCAGGGCCCACTCAATGCCATTGACTTGTGTGCCATCTTGCACATACTATGTCACC 992  
258 ValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeu 277  
993 ATTTTCTCCAGAAATCCAAAGAGCGTGCTCGCAATTCAGAAATGTCGCCGCGGTGTC 1052  
278 ArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGly 297  
1053 CAGATCTTCGCATCATGCGAATTCCTCCGATCCTTAAGCTTCACGCCACTCCACTGGC 1112  
298 LeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuVal 317  
1113 CTCAGTCTCTGGGCTTCACTTTGCGAGAGAGCTACAATGAGTGGGCTTGTCTCATCTCTC 1172  
318 PheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuHisGlyLeu 337  
1173 TTCTTCCCATGGGCATATGATCTTCTCCAGCCTTCTCTTCTGTGTGAGAAGGATGAG 1232  
338 AspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIle 357  
1233 GAC-----GACACCAAGATTCAAAAGCATCCACGCTTCTTCTGTGGGGCCACC 1280  
358 IleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIle 377  
~1281 ATCACCATGACTACTGTGTGGATGAGAGACATCTACCCCAAGACTCTCTCTGGGGAAATTT 1340  
378 LeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIle 397  
1341 GTTGGGGGACTCTGCTGATGTCAGGAGTCTGCTGTGATGCTCTTCCCATCCCATCATC 1400

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QY      398 TyrHisSerPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArg 417
Db      ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
          1401 GTCAATAAATCTCTCGAGTTCTATAGGAGCAGACAGAGAAGCAATCAACCG 1460
QY      418 SerLeuSerThrGlu 422
Db      ::::|||||
          1461 CGAGAGGCTCTGGAG 1475

RESULT 6
US-10-815-297-2
; Sequence 2, Application US/10815297
; GENERAL INFORMATION:
; APPLICANT: Jsgla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: Kv10.1, a Novel Voltage-Gated Potassium Channel From
; TITLE OF INVENTION: Human Brain
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/10/815,297
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/833,466
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human alpha subunit of voltage-gated potassium
; OTHER INFORMATION: channel Kv10.1 coding sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1638)
; OTHER INFORMATION: Kv10.1
US-10-815-297-2

Alignment Scores:
Pred. No.:           4, 85e-68           Length:           1638
Score:              636.50             Matches:            148
Percent Similarity: 53.96%             Conservative:       77
Best Local Similarity: 35.49%          Mismatches:        159
Query Match:         28.74%            Indels:            33
DB:                  6                 Gaps:              10

US-10-016-647-2 (1-425) x US-10-815-297-2 (1-1638)

QY      13 LeuAsnValGlycylalaArgTyrSerLeuSerArgGluLeuLysAspPheProLeu 32
Db      ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
          301 GTGAAGCTGGTGCCACAGCTACCAGCTGGACTCTGGAGCTGCCGCCTTCCCCAAG 360
QY      33 ArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAsp 52
Db      ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
          361 ACCGGCTAGTCGCTGCCACCTCCACAGCGCGAGCCAGCTAACGCTGTGGCAC 420
QY      53 AspTyrAspArgGluArgAsnGluTyrPheAspArgHisSerGluAlaPheGlyPhe 72
Db      :|||:::|||||:::|||||:::|||||:::|||||:::|||||
          421 GACTACGAGGAGCAGACAGCAATACTTCTTCGACCGGACCCGGCCGCTTCCACGCTG 480
QY      73 IleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeu 92
Db      :|||:::|||||:::|||||:::|||||:::|||||:::|||||
          481 GTCTACAATTCTACCTGTC---GGGGTCTGCTGCTCGACGGCGTGTGCCGCG 537
QY      93 SerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCys 112
Db      :|||:::|||||:::|||||:::|||||:::|||||:::|||||
          538 CGCTTCTCGAGGAGCTGGGCTACTCGGGCGTGGCGCTCAAGTACACGCCACCGCTGCTGC 597
QY      113 -----GlnArgArg-----LeuAspAspArgMetSerAspThrTyrThr 125
Db      :|||:::|||||:::|||||:::|||||:::|||||:::|||||
          598 CGCATCTGCTTCGAGGAGCGGCGCAGCAGCTAGCGNACGGCTCAAGATCCAGCACGAG 657
QY      126 PheTyrSer-----AlaAspGluProGlyValLeuGlyArgAspGluAlaArgPro 142

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Db	658	CTGCGCGCGCAGGCGCAGGTCTGAGAGGCGGAGAACTCTTCCGCGACATGCGCTTCTAC	717
Qy	143	GlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgAthrPheGlu	162
Db	718	GGC-----CCGACGCGCGC-----CGCTCTCGGAACCTCATGGAG	753
Qy	163	GluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIle	182
Db	754	AAGCAATTCCTCGTGGCGGCCCAAGCCATCGGGTGGCGTCCAGCACTTCGTGCTC	813
Qy	183	ValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAasp	202
Db	814	GTCTCCGTGGTGGCGCTCAACACCGTGGAGGAGATGCAGAGCACTCGGGCGAG	873
Qy	203	AsnArgSerLeuAspAspArgSerArgIle-----IleGluAlaIleCysIleGly	219
Db	874	GGCGAGGCGGCCAGACCTCGCGCCCATCTCTGGAGCACGTGGAGATGCTGTGATGGC	933
Qy	220	TrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheVal	239
Db	934	TTCTTCACGCTCGAGTACCTGCTCGCTAGCTCCAGCCGCGACCTGAGCGCTTCGCG	993
Qy	240	LysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeu	259
Db	994	CGACGCCCTCAACCTGGTGGACCTGGTGGCCATCTCGCGCTTACCTTCAGCTGCTG	1053
Qy	260	MetThrValPheThrGlyGluAsnSerGln-----LeuGluArg	272
Db	1054	CTCGAGTCTTCACGGCGGCGGGCCACCAACGCGCGCAGCGGTGGCGAGCGTGGTAAG	1113
Qy	273	AlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAla	292
Db	1114	GTGGGTGAGGTGTTGCGCGTTCATCGCGCTCATGCGCATCTTCCGCATCTCTCAAGCTGCGC	1173
Qy	293	ArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMet	312
Db	1174	CGGCATCTCCACCGACATCGGTGCGCTTCGGCTTCAGCTGCGCCAGTGTACACAGAGTG	1233
Qy	313	ValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeu	332
Db	1234	GGCTGCGCTGCTGCTTCATCGCCATCGGCATCTTCATCTTCTCTGGCGGTGCTACTCT	1293
Qy	333	LeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla	352
Db	1294	GTGAGGAC-----GATGCCGACGACCAC-----TTCATCATCTCCCACTCC	1341
Qy	353	CysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThr	372
Db	1342	TGGTGGTGGCGCGGTGAGCATCTCCACCGTGGCTACGGAGACATGTACCCAGAGACC	1401
Qy	373	ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeu	392
Db	1402	CACCTGGCGAGTTTTTGGCCCTCTCTGCAATCTGCTTTGGATCATCTCAACGGGATG	1461
Qy	393	ProIleThrPheIleTyrHisSerPheValGlnCystyrHisGluLeuLys	409
Db	1462	CCCATTTCCATCTCTCAACAAAGTTTTCTCATTTACTACCAAGCTGAAC	1512

## RESULT 7

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US-10-815-297-1
; Sequence 1, Application US/10815297
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: Kv10.1, a Novel Voltage-Gated Potassium Channel From
; TITLE OF INVENTION: Human Brain
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/10/815,297
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/833,466
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793

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; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human alpha subunit of voltage-gated potassium
; OTHER INFORMATION: channel Kv10.1
; NAME/KEY: CDS
; LOCATION: (151)..(1788)
; OTHER INFORMATION: Kv10.1
US-10-815-297-1

Alignment Scores:
Pred. No.: 7,27e-68 Length: 2103
Score: 636.50 Matches: 148
Percent Similarity: 53.96% Conservative: 77
Best Local Similarity: 35.49% Mismatches: 159
Query Match: 28.74% Indels: 33
DB: Gaps: 10

US-10-016-647-2 (1-425) x US-10-815-297-1 (1-2103)
QY 13 LeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeu 32
Db 451 GTGAACGTGGTGGCCACACCTACACCTAGCTGGACTACTGCGAGCTGGCGGCTTCCCCAAG 510
QY 33 ArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAsp 52
Db 511 ACGCGCTAGGTCGCTGGCCACTCTCCACCAGCGCCAGCGCCAGCTAAGCCTGTGGCAC 570
QY 53 AspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPhe 72
Db 571 GACTACGAGGAGCAGACAGCAATACCTCTTCGACCGCAGCCCGCGCTCTTCCAGCTG 630
QY 73 IleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeu 92
Db 631 GTCTACAATTCTACCTGTCTCC--GGGGTCTCTGTGTCTCGACGGGTGTGTGTCGCGC 687
QY 93 SerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCys 112
Db 688 CGCTTCCTGAGGAGCTGGGCTACTCGGGGCTCGGCTCAAGTAGTACACGCCACGCTGTGTC 747
QY 113 -----GlnArgArg-----LeuAspAspArgMetSerAspThrTyrThr 125
Db 748 CGCATCTGCTTCAGGAGAGCGCGCAGCAGCTGAGCGAAGCGCTCAGATCCACACGAG 807
QY 126 PheTyrSer-----AlaAspGluProGlyValLeuGlyArgAspGluAlaArgPro 142
Db 808 CTGCGCGCGCAGCGCGAGGTCGAGGAGCGCGAGGAACCTCTTCGCGCATCGCGCTTCTAC 867
QY 143 GlyGlyAlaGluAlaProSerArgArgTrpLeuGluArgMetArgThrPheGlu 162
Db 868 GGC-----CCGCGAGCGCGC-----CGCTCTCGAACCTCATGGAG 903
QY 163 GluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIle 182
Db 904 AAGCAATCTCTTCGGTGGCGCGCAGAGCCATCGGGGTGGCGTCCAGCACCTTCGTGTC 963
QY 183 ValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAsp 202
Db 964 GTCTCGGTGTGGCTGGCGCTCAACACCGTGGAGGATGTCAGCAGCAGCTCGGGGAG 1023
QY 203 AsnArgSerLeuAspArgSerArgIle-----IleGluAlaIleCysIleGly 219
Db 1024 GCGCAGGGCGCCAGACCTTCGGGCCCATCTTGGAGCACCTGGAGATGTGTGTCATGGC 1083
QY 220 TrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheVal 239
Db 1084 TTCTTCAGCTCGAGTACCTGCTCGGCTAGCCTCCACGCCGCCAGCTGAGCGGCTTCGCG 1143

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Qy 240 LysArgProLeuAsnIleLeuAspLeuLeuAlaIleThrProTyrTyrIleSerValLeu 259
Db 1144 CGAGCGCCCTCAACTGTGGAGCCTGTGGCCATCTCGCGCTCTACCTTTCAGCTGTG 1203
Qy 260 MetThrValPheThrGlyGluAsnSerGln-----LeuGlnArg 272
Db 1204 CTGAGTGTTCACGGCGAGGGCCACCAACCGCGGACAGCGTGGCGAGCGTGGTAAG 1263
Qy 273 AlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAla 292
Db 1264 GTGGTTCAGGTGTGGCGTCATCGCGCTCATCGCATCTTCGGCATCTCAAGCTGGCG 1323
Qy 293 ArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTrpArgGluMet 312
Db 1324 CGGCATCCACCGGACTGCTGCTTGGCTTCACGCTGCGCAGTGTACAGCAGGTTG 1383
Qy 313 ValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeu 332
Db 1384 GGCTGCTGCTCTTCATCGCATGGCATCTTCATCTTCTCGGCTGCTACTCT 1443
Qy 333 LeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla 352
Db 1444 GTGGAGCAC-----GATGGCCAGACCAAC-----TTCACTACCATCCCTCC 1491
Qy 353 CysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThr 372
Db 1492 TGTGTGGCGCGGTGGAGCATCTCCACGCTGGGTACGGAGACATGTACCCAGAGACC 1551
Qy 373 ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeu 392
Db 1552 CACCTGGCGAGGTTTTTGGCTTCTCTGCTGCTGCTTTTGGGATCATCTTCAACGGGATG 1611
Qy 393 ProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
Db 1612 CCCATTTCATCTCTACAAAGTTTTCGTATTACTACAGCAAGCTGAAG 1662

RESULT 8
PCT-US04-03417-9
; Sequence 9, Application PC/TUS0403417
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28859, 53659, 64549,
; TITLE OF INVENTION: 9455, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; FILE REFERENCE: MPI03-015
; CURRENT APPLICATION NUMBER: PCT/US04/03417
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15

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; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (381)...(1952)
PCT-US04-03417-9

Alignment Scores:
Pred. No.: 6.92e-60 Length: 3303
Score: 574.50 Matches: 138
Percent Similarity: 53.22% Conservative: 85
Best Local Similarity: 32.94% Mismatches: 137
Query Match: 25.94% Indels: 59
DB: 1 Gaps: 12

US-10-016-647-2 (1-425) x PCT-US04-03417-9 (1-3303)
Qy 11 ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe 30
Db 540 GTGTGTATCAATCTCCGGCTGCTCGAGACGCGAGCTGAAGACCTTTGCCAGTTC 599
Qy 31 ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
Db 600 CCC-----GAGACGCTGCTGGCGACCCCAAGCGCGCC----- 632
Qy 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
Db 633 ATGAGTACTTCGACCGCTCCGCAACAGTACTTCTTCAGCGCAACCGCCAGCTTC 692
Qy 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
Db 693 GACGCCATCTCTACTACTATCATCGTGGGGGCGCATCCGC-----CGCGCGGTCAACGTG 749
Qy 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
Db 750 CCATCGACATTTCTCCGAGGATCCGCTTC----- 782
Qy 111 CysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
Db 783 -----TACCAGCTGGGAGGAGGCCATGGAGAAGTTC-----CGCGAG 821
Qy 131 GluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaProSer 150
Db 822 GACGAGGCTTCCG-----CGGAGGAGGAGCGCGCC-----TTGCCCGCG 863
Qy 151 ArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAla 170
Db 864 CGCGACTTCCAGCGCCAGGTGTGCTCTCTCGAGTACCCCGAGAGCTCCGCGCGCGCC 923
Qy 171 GlnIleLeuAlaSerValSerValPheValPheValIleValSerMetValValLeuCysAla 190
Db 924 CGGGGATCCGCATCGGTGCTCGTCTGCTCATCTCTCATCTCTCATCTCTCTCTCTGCTG 983
Qy 191 SerThrLeuProAspTrpArg----- 197
Db 984 GAGACGCTGCGGAGTTCCCGGACGAGAGACTACCCCGCTCGAGCTCGCAGGACTCA 1043
Qy 198 -----AsnAlaAlaAspAsnArg-----SerLeuAspAsp 208
Db 1044 TTCGAGCAGCGCGCAACAGCAGCTCGGGTCCCGCGAGAGCCCTCCAGCTTCTCCGAT 1103
Qy 209 ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArg 228
Db 1104 CCCTTCTCTGTTGGAGAGCGTGTGCATCATCTGTTCTCTCTCGACTGCTGGTGG 1163
Qy 229 PheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeu 248

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (381)...(1952)
US-10-772-636-9

Alignment Scores:
Pred. No.: 6,92e-60 Length: 3303
Score: 574.50 Matches: 138
Percent Similarity: 53.22% Conservativeness: 85
Best Local Similarity: 32.94% Mismatches: 137
Query Match: 25.94% Indels: 59
DB: 6 Gaps: 12

US-10-016-647-2 (1-425) x US-10-772-636-9 (1-3303)
QY 11 ValValLeuAsnValGlyAlaArgTy-SerLeuSerArgGluLeuLeuLysAspPhe 30
DB 540 GTGGTCATCAATCTCGGGCTCGCTTCGAGACGCGAGTGAAGACCCITTCGCGATTC 599
QY 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuVal 50
DB 600 CCC-----GAGACGCTCTCGGGCAGCCCAAGCGCGC----- 632
QY 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
DB 633 ATGAGGTACTTCGACCGCTCCGACACGAGTACTTCTTCGACCGCAACCGCGCGATTC 692
QY 71 GlyPheLeuLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
DB 693 GACGCCATCTCTACTACTATCATGTCGGGGCGGCATCCGCGC---CGGCCGCTCAACGTG 749
QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
DB 750 CCCATCGACATTTCTCCGAGAGATCCGCTTC----- 782
QY 111 CysCysGlnArgLeuAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
DB 783 -----TACCAGCTGGGGAGGAGCCATGGAAGTTC-----CGCGAG 821
QY 131 GluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSer 150
DB 822 GACGAGGGCTTCCTG---CGGGAGGAGGAGCGGCC-----TTGCCCGCGC 863
QY 151 ArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAla 170
DB 864 CGGACTTCCAGCGCCAGGTGTGCTCTTCAGTACCCCGAGAGCTCGGGCGCGGCC 923
QY 171 GlnLeuAlaSerValSerValValPheValLeuValSerMetValValLeuCysAla 190
DB 924 CGGGCATCGCATCGTGTGCTGTGTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 983
QY 191 SerThrLeuProAspTrpArg----- 197
DB 984 GAGACGCTGCCGGAGTTCGCGAGAGGAGTACCCCGCTCGAGCTCGAGCTCGAGACTCA 1043
QY 198 -----AsnAlaAlaAlaAspAsnArg-----SerLeuAspAsp 208
DB 1044 TTCGAGCGAGCGCGCAACAGCACGCTCGGGGTCCCGCGAGGAGCTTCAGCTTCCTCCGAT 1103
QY 209 ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArg 228
DB 1104 CCCCTTCTTCGTGGGAGACGCTGTGTCATCATCTGTGTTCTCTTCGAACTCTCTGTCGGG 1163
QY 229 PheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeu 248
DB 1164 TTCCTCGCTTCTCTAGCAAGCCACCTTCTTCGGAACATCATCAACCTGATCGACATT 1223

```

RESULT 9

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US-10-772-636-9
; Sequence 9, Application US/10772636
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118', 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 13290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; FILE REFERENCE: MPI03-015PIRNOWNIM
; CURRENT APPLICATION NUMBER: US/10772,636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10

```

```

Qy 249 LeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGlu---Asn 267
Db 1224 GTGGCCATCATCTCTTTATCTACCTCTGGGTACCGAGCTGGCCGCAACGACAGGCAAT 1283
Qy 268 SerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrp 287
Db 1284 GGACAGAGGCCCATGCTCTGGCCATCTCTGAGGTATCTCCGCTGGTGGAGGCTCTCCGC 1343
Qy 288 ValIleLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArg 307
Db 1344 ATCTCAAGCTGTGCGCCACTCAAGGCGCTGCAGATCTCGGGCAACGCTGAAGCG 1403
Qy 308 CysTyrArgGluMetValMetLeuValPheIleCysValAlaMetAlaIlePheSer 327
Db 1404 TCCATGCGGAGCTGGGATTCATCTCTCTCTTTATGGGTCTATCTTTCTCC 1463
Qy 328 AlaLeuSerGlnLeuLeuHisGlyLeuAspLeuGlnThrSerAsnLysAspPheThr 347
Db 1464 AGCGCGTCTACTTTGCCGAG-----GCAGAGCAGCCCACTTCAGGT-----TTCAGC 1511
Qy 348 SerIleProAlaLysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAsp 367
Db 1512 AGCATCCCGGATGCTCTCTGGCGAGTGTAAACCATGACACAGTGGGTACGCGCAT 1571
Qy 368 MetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIle 387
Db 1572 ATGACCCAGTGCACCATAGGGGCGAGATGTGGATCTCTGTGCCATCGCGGTGTC 1631
Qy 388 ValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHis 406
Db 1632 TTGACCATCGCATTTGCCAGTTCGCGTATGTTTCCAACTTCAATTACTTCTACAC 1688

RESULT 10
PCT-US04-02851-9
; Sequence 9, Application PC/TUS0402851
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21495, 27410, 38554, 38555, 55063, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MPI03-012
; CURRENT APPLICATION NUMBER: PCT/US04/02851
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4234
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (853) ... (2452)
PCT-US04-02851-9

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Alignment Scores: 7e-56 Length: 4234
Pred. No.: 543.50 Matches: 144
Score:

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Percent Similarity: 45.45% Conservative: 71
Best Local Similarity: 30.44% Mismatches: 149
Query Match: 24.54% Indels: 109
DB: 1 Gaps: 12

US-10-016-647-2 (1-425) x PCT-US04-02851-9 (1-4234)

Qy 4 GlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAlaArgTyr 20
Db 959 GGGGCGGGGCTCTCTGTAGTAGGAGCGGTGTGATCAATATCTCCGGCTCGGCTTT 1018
Qy 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
Db 1019 GAGACACAATTCGCGACCCCTGCTCTGTTCCG-----GACAGCTGCTCGGA 1066
Qy 41 CysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGlu 60
Db 1067 GACCTGCGCGCGA-----GTCCGCTTCTCGACCCCTGAGGAACGAG 1111
Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
Db 1112 TACTTCTTCGACCCGCAACCGGCCCATCTCTACTACTACCATCTCTGGG 1171
Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 1172 GGCCGCTGCGG---AGGCCGCTCAACGTCGCCCTGGACATTTTCTCGAGGAGATC--- 1225
Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
Db 1226 -----CGCTTCTACCAGTGGG 1243
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeu-----GlyArg 137
Db 1244 GACGAGCCCTGGCGGCTTCCGGGAGGACGAG---GGCTGCTGCCGAGGAGTGGCGAG 1300
Qy 138 AspGluAlaArgProGlyGlyAlaGluAlaProSerArgArgTrpLeuArgMet 157
Db 1301 GACGAG-----AAGCCGCTGCGCTTCCAGCCCTTCCAGCCGCGAGTG 1342
Qy 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer 177
Db 1343 TGGCTGCTCTTTGAGTACCAGAGAGCTCTGGGCGCGCCAGGGGCATCGCATCTCTCC 1402
Qy 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
Db 1403 GTGTGTGTCATCTCTCATCTCCATAGTCATCTTTGCTGAGACCTTACCCGAGTTCGCT 1462
Qy 198 AsnAlaAlaAlaAspAsnArgSer----- 205
Db 1463 -----GTAGATGTCGAGGTGGAAACAATGGTGTGTGAGTCGAGTCTCCCGAGTT 1513
Qy 205 ----- 205
Db 1514 TCCAGGGGAGTCAGGAGGAGGAGGAGATGAAGACGATTCTTACACATTTTCATGCGC 1573
Qy 205 ----- 205
Db 1574 ATCACCCCTGGGAAATGGGACCGGGGCTCTCTCTCACTAGTACTCTTGGGGGCTCC 1633
Qy 206 ---LeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224
Db 1634 TTCTTTACAGACCCCTCTCTTCTGTTGGAGACGCTGTGCATTGTCTGTTTCTTTTGG 1693
Qy 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
Db 1694 CTCTGTGTGGCTTCTCCGCTGCCCTAGCAAGCCGCTCTTCTTCCGAAACATCATGAAC 1753
Qy 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264
Db 1754 ATCATTGACTTGTGGCTATCTTCCCTTACTCATCCCTGGGCACTGAGCTGGTGCAG 1813
Qy 265 -----GlyGluAsnSerGlnLeuGlnArgAla 273

```



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Db 1814 CAGCAGGAGCAACAGCCAGTCGGAGGAGCGGCCAGAAATGGCGAGCCATGTCC 1873
Qy 274 GlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArg 293
Db 1874 CTGGCCATCCTCCGAGTCATCCGCTGGTCGGGTTCGGCATCTTCAAGCTCTCCCGC 1933
Qy 294 HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyArgGluMetVal 313
Db 1934 CACTCAAGGGGCTGCAGATCTCGGCAAGACCTTGCAGCGCTCCATGAGGAGCTGGG 1993
Qy 314 MetLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
Db 1994 CTGCTCATCTTCTCTCTTCATCCAGGTCACTCTTCAGGCGCGCTTACTTCGCA 2053
Qy 334 GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db 2054 GAG-----GCTGACCATGACGATTCGCTTTTCCAGCATCCCGATGCCCTTC 2101
Qy 354 TrpTrpValIleSerMetThrThrValGlyTyrGlyAspMetTyProIleThrVal 373
Db 2102 TGGTGGCAGTGGTTACATGACCAACGCTAGGTACGGGGACATGATCCCATGACTGTG 2161
Qy 374 ProGlyArgIleLeuGlyValCysValValSerGlyIleValLeuLeuAlaLeuPro 393
Db 2162 GGGGAAAGATCGTGGCTCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2221
Qy 394 IleThrPheIleTyHisSerPheValGlnCysTyHis 406
Db 2222 GTGCCGTCATCGTCTCCAACCTCACTACTTCTACCAC 2260

RESULT 11
US-10-768-158-9
; Sequence 9, Application US/10768158
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21425, 27410, 38554, 38555, 55063, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MPI03-012PIRNOMIN
; CURRENT APPLICATION NUMBER: US/10768,158
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4234
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (863)...(2452)
US-10-768-158-9
Alignment Scores:
Pred. No.: 7e-56 Length: 4234
Score: 543.50 Matches: 144
Percent Similarity: 45.45% Conservative: 71
Best Local Similarity: 30.44% Mismatches: 149
Query Match: 24.54% Indels: 109
```

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DB: 6 Gaps: 12
US-10-016-647-2 (1-425) x US-10-768-158-9 (1-4234)
Qy 4 GlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAlaArgTyr 20
Db 959 GGGGGGGGGGGCTGTGTAGTAGCGAGCGGTGTGATCAATATCTCCGGGCTGGCGTTT 1018
Qy 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
Db 1019 GAGACACAATTGGCCACCTGTGCTGTTTCCG-----GACACGCTGCTCGGA 1066
Qy 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
Db 1067 GACCTCGCCGGCGA-----GTCCGCTTCTTCGACCCCTCGAGAGAGAG 1111
Qy 61 TyrPhePheAspArgHisGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
Db 1112 TACTTCTTCGACCGCAACCGCCAGCTTCGACGCCATCTCTACTACTACCATCTGGG 1171
Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 1172 GCGCGCTGCGG---AGGCGGTCAAGTGCCTCGACATTTTCTTGGAGGAGATC-- 1225
Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120
Db 1226 -----CGCTTCTACCAGCTGGG 1243
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspLupProGlyValLeu-----GlyArg 137
Db 1244 GACGAGCCCTGGCGGCTTCGGGAGGAGGAG---GGCTGCTTCCCGAAGGTGGCGAG 1300
Qy 138 AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTyrLeuGluArgMet 157
Db 1301 GACGAG-----AAGCGCTGCCCTCCAGCCCTTCCAGCGCCAGGTG 1342
Qy 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValser 177
Db 1343 TGGCTGCTCTTGTAGTACCCAGAGAGCTTGGGCGCGCCAGGCGCATCGCTCTCC 1402
Qy 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
Db 1403 GTGTTGTGTCTCTCTCATCTCATAGTACTCTTTTSCCTGGAGACCTTACCCAGTCCGT 1462
Qy 198 AsnAlaAlaAlaAspAsnArgSer----- 205
Db 1463 -----GTAGATGTCGAGGTGGAAACAATGGTGTGTGAGTCGAGTCTCCCGAGTT 1513
Qy 205 ----- 205
Db 1514 TCCAGGGGAGTCAGGAGGAGAGAGGAGATGAAGACGATTCTCTACACATTTTCATGGC 1573
Qy 205 ----- 205
Db 1574 ATCACCCTGGGAAATGGGAGCGGGGCTCTCTCCTACCTACTCTTTGGGGGCTCC 1633
Qy 206 ---LeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTyrPheThrAlaGlu 224
Db 1634 TTCATTACAGACCCCTTCTTCTGTGTGAGAGCGGTGTGATTGTCTGGTTTCACTTTTGG 1693
Qy 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
Db 1694 CTCCTGTGTCGCTTCTCCGCTGCTAGCAAGCGGCTTCTTCCGGAACCATCATGAAC 1753
Qy 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264
Db 1754 ATCATTTGCTGGTGGCTATTTCTCCCTACTCTCATCCCTGGGCACTGAGCTGGTGAC 1813
Qy 265 -----GlyGluAsnSerGlnLeuGluAlaArg 273
Db 1814 CAGCAGGAGCAGCAACAGCCAGCCAGTGGAGGAGCGGCCAGAAATGGCGAGCCATGTCC 1873
Qy 274 GlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArg 293
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Db 1874 CTGGCCATCTCCGAGTCATCCGCTGGTCCGGGTGTCCGCATCTTCAAGCTCTCCCGC 1933
Qy 294 HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuHisArgCysTyrArgGluMetVal 313
Db 1934 CACTCCAAGGGGCTGCAGATCTTGGGCAAGACCTTGCAGGCTCCATGAGGGAGCTGGG 1993
Qy 314 MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeu 333
Db 1994 CTGCTCATCTTCTTCCTTCCTTCATCGGGGTCTATCTTCTCCAGTCGCGCTACTTCGCA 2053
Qy 334 GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db 2054 GAG-----GCTGACGATGACGATTCGCTTTTCCAGCATCCCGGATGCTTC 2101
Qy 354 TrpTrpValIleIleSerMetThrValGlyTyrGlyAspMetTyrProIleThrVal 373
Db 2102 TGTGGGCAAGTGTACAAATGACACCGTAGTACGGGACATGTACCCCATGACTGTG 2161
Qy 374 ProGlyArgIleLeuGlyValCysValValSerGlyIleValLeuLeuAlaLeuPro 393
Db 2162 GGGGGAAGATGTGGGCTCGCTGTGTGTCATCGTGGGTCTCCATTCGCTTCGCT 2221
Qy 394 IleThrPheIleTyrHisSerPheValGlnCysTyrHis 406
Db 2222 GTGCCCGTCATCGTCTCCAACTTCAACTACTTCTACCAC 2260

RESULT 12
US-10-796-280-12293/c
; Sequence 12293, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12293
; LENGTH: 64206
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-12293

Alignment Scores:
Pred. No.: 7,45e-53 Length: 64206
Score: 534.50 Matches: 105
Percent Similarity: 65.10% Conservative: 61
Best Local Similarity: 41.18% Mismatches: 84
Query Match: 24.13% Indels: 5
DB: 6 Gaps: 2

US-10-016-647-2 (1-425) x US-10-796-280-12293 (1-64206)
Qy 169 AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188
Db 62556 TCTTCACAGATCTTGCATATATTTCCATCATGTTCTATCGTCTCTCCACCATGCGCTG 62497
Qy 189 CysAlaSerThrLeuProAspTrpArgAsnAlaAlaAspAsnArgSerLeuAspAsp 208
Db 62496 TCCTCAACAGCTGCTGAGCTACAGAGCTCGATGAGTTCGGCCAGTCCACAGACAC 62437
Qy 209 ---ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVal 227
Db 62436 CCCAGCTGCCGCCAGCTGAGGCGCGTGTGTCATGCTGATGTTTCCATGAGTACCTGTG 62377
Qy 228 ArgPheIleValSerLysAsnLysCysGluPheValIleArgProLeuAsnIleIleAsp 247
Db 62376 AGTTTCTCTCTCGCCCAAGAGTGAAGTCTTCAAGGGGCCACTCATGCCATTGAC 62317
Qy 248 LeuLeuAlaIleThrProTyrIleSerValLeuMetThrValPheThrGlyGluAsn 267

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Db 62316 TTGTTGGCCATCTCCCATATATGTACCATTTTCTCCACGAATCCACAGAGCGTG 62257
Qy 268 SerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrp 287
Db 62256 CTGCAATTCAGAAATGTCCGCGGTGTGTGCAGATCTTCGCGCATCATCGCAATTCGCG 62197
Qy 288 ValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArg 307
Db 62196 ATCTTAAGCTGACGCGCATCCACTGGCTCCAGTCTCTGGGCTTCACATTTCCGGAGG 62137
Qy 308 CysTyrArgGluMetValMetLeuValPheIleCysValAlaMetAlaIlePheSer 327
Db 62136 AGCTACATGAGTGGGCTTCTCATCTCTCTTCTTCCATGGCATTATGATCTTCTCC 62077
Qy 328 AlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThr 347
Db 62076 AGCCTGTCTCTTGTGTGAGAGGATGAGGAC-----GACACCAAGTTCAAA 62029
Qy 348 SerIleProAlaAlaCysTyrTrpValIleIleSerMetThrValGlyTyrGlyAsp 367
Db 62028 AGCATCCAGGCTCTTCTGTGTGGCCACCATCACCATGACTCTTGGGTATGGAGAC 61969
Qy 368 MetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIle 387
Db 61968 ATCTACCCCAAGACTCTCTGGGGAATTTGTGGGAGACTCTGCTGCATTGCAGGAGTC 61909
Qy 388 ValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGlu 407
Db 61908 CTGTGATGTCTTCCATCCCATCTCATTAATCTCTGAGTCTCTATAAGGAG 61849
Qy 408 LeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGlu 422
Db 61848 CAGAAGACAGAGAGAAAGCAATCAACGCGGAGAGCTCTGGAG 61804

RESULT 13
US-10-796-280-12305/c
; Sequence 12305, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12305
; LENGTH: 68305
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-12305

Alignment Scores:
Pred. No.: 8,24e-53 Length: 68305
Score: 534.50 Matches: 105
Percent Similarity: 65.10% Conservative: 61
Best Local Similarity: 41.18% Mismatches: 84
Query Match: 24.13% Indels: 5
DB: 6 Gaps: 2

US-10-016-647-2 (1-425) x US-10-796-280-12305 (1-68305)
Qy 169 AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188
Db 62637 TCCTCAAGATCTTGCATATATTTCCATCATGTTCTATCGTCTCTCCACCATGCGCTG 62578
Qy 189 CysAlaSerThrLeuProAspTrpArgAsnAlaAlaAspAsnArgSerLeuAspAsp 208
Db 62577 TCCTCAACAGCTGCTGAGCTACAGAGCTCGATGAGTTCGGCCAGTCCACAGACAC 62518
Qy 209 ---ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVal 227
Db 62517 CCCAGCTGCCGCCAGCTGAGGCGCGTGTGTCATGCTGATGTTTCCATGAGTACCTGCTG 62458

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Qy 228 ArgPheileValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleileAsp 247  
Db 62457 AGTTCTCTCTCGCCCAAGAGTGGAGTTCTTCAAGGCGCCCACTCAATGCCATTGAC 62398  
Qy 248 LeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsn 267  
Db 62397 TTGTTGGCCATTCTGCGCATACTATGTCACCACTTTTCTCCTCAAGCAATCCCAAGAGCGTG 62338  
Qy 268 SerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuMetMetArgIlePheThr 287  
Db 62337 CTGCAATTCAGAAATGTCGCGCGTGGTCCAGATCTTCCGATCATCGCAATTCCTCCG 62278  
Qy 288 ValIleLeuLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArg 307  
Db 62277 ATCCTTAAGCTTGCAGCCCACTCCACTGGCCCTCCAGTCTCTGGGCTTCACITTTGGGAGG 62218  
Qy 308 CysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSer 327  
Db 62217 AGCTCAATGAGTTGGGCTTGTCTATCTCTCTCTTCCATGGCATATGATATCTCTCC 62158  
Qy 328 AlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThr 347  
Db 62157 AGCTTGTCTCTTCTGCTGAGAAGGATGAGGAC-----GACACCAAGTTCAA 62110  
Qy 348 SerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAsp 367  
Db 62109 AGCATCCCAAGCTTCTTCTGGTGGGCCACCATCATCATGACTACTGTGGGTATGGAGAC 62050  
Qy 368 MetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIle 387  
Db 62049 ATCTACCCCAAGCTCTCTGGGAAATTTGTTGGGACTCTGTGCAATTCAGAGATC 61990  
Qy 388 ValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGlu 407  
Db 61989 CTGGTGTGCTCTTCTCCATCCCATCATCATGCTCAATAACTTCTGAGTCTATAAGGAG 61930  
Qy 408 LeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGlu 422  
Db 61929 CAGAGAGACAGGAGAAAGCAATCAACCGCGAGGAGCTCTGGAG 61885

## RESULT 14

US-10-796-280-12388

; Sequence 12388, Application US/10796280

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: STENOIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001510

; CURRENT APPLICATION NUMBER: US/10/796,280

; CURRENT FILING DATE: 2004-03-10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12388

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-796-280-12388

## Alignment Scores:

Pred. No.:	2,16e-52	Length:	123593
Score:	534.50	Matches:	105
Percent Similarity:	65.10%	Conservative:	61
Best Local Similarity:	41.18%	Mismatches:	84
Query Match:	24.13%	Indels:	5
DB:	6	Gaps:	2

US-10-016-647-2 (1-425) x US-10-796-280-12388 (1-123593)

Qy 169 AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188  
Db 113659 TCCTCAGATCTCTGCCAATAATTCATCATGCTTCATCGCTCTCCACCATTTGCCCTG 113718

Qy 189 CysAlaSerThrLeuProAspTyrArgAsnAlaAlaIleAspIleArgSerLeuAspAsp 208  
Db 113719 TCCTCAACACGCTGCTGAGCTACAGAGCTCGATGAGTTCGCCCATCCACAGACAAC 113778  
Qy 209 --ArgSerArgIleIleGluAlaIleCysIleGlyTyrPheThrAlaGluCysIleVal 227  
Db 113779 CCCAGCTGCCACAGTGGAGCGGTGTCATGCGATGGTTCACCATGGAGTACCTGCTG 113838  
Qy 228 ArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleileAsp 247  
Db 113839 AGGTTCTCTCTCGCCCAAGAGTGGAGTCTTCTCAAGGCGCCCACTCAATGCCATTGAC 113898  
Qy 248 LeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsn 267  
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Qy 268 SerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuMetMetArgIlePheThr 287  
Db 113959 CTGCAATTCAGAAATGTCGCGCGTGGTCCAGATCTTCCGATCATCGCAATTCCTCCG 114018  
Qy 288 ValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArg 307  
Db 114019 ATCCTTAAGCTTGCAGCCCACTCCACTGGCCTCCAGTCTCTGGGCTTCACITTTGGGAGG 114078  
Qy 308 CysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSer 327  
Db 114079 AGCTCAATGAGTTGGGCTTGTCTATCTCTTCCATGGCATATGATATCTCTCC 114138  
Qy 328 AlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThr 347  
Db 114139 AGCTTGTCTCTTCTGCTGAGAAGGATGAGGAC-----GACACCAAGTTCAA 114186  
Qy 348 SerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAsp 367  
Db 114187 AGCATCCCAAGCTTCTTCTGGTGGGCCACCATCATCATGACTACTGTGGGTATGGAGAC 114246  
Qy 368 MetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIle 387  
Db 114247 ATCTACCCCAAGACTCTCTGGGAAATTTGTTGGGAGCTCTCTGCTGATTCGAGGATC 114306  
Qy 388 ValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGlu 407  
Db 114307 CTGGTGTGCTCTTCCATCCCATCCCCATCATCTCAATAACTTCTCTGAGTCTATAAGGAG 114366  
Qy 408 LeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGlu 422  
Db 114367 CAGAGAGACAGGAGAAAGCAATCAACCGCGAGGAGCTCTGGAG 114411

## RESULT 15

US-60-545-213-3833

; Sequence 3833, Application US/60545213

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William Martin

; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; FILE REFERENCE: Target Genes

; FILE REFERENCE: AM101083 (031896-042099)

; CURRENT APPLICATION NUMBER: US/60/545,213

; CURRENT FILING DATE: 2004-02-18

; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3833

; LENGTH: 1400

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-545-213-3833

## Alignment Scores:

Pred. No.:	9,65e-50	Length:	1400
Score:	487.50	Matches:	112
Percent Similarity:	56.48%	Conservative:	58
Best Local Similarity:	37.21%	Mismatches:	115
Query Match:	22.01%	Indels:	16

DB:		7	Gaps:	5
US-10-016-647-2	(1-425)	x US-60-545-213-3833	(1-1400)	
QY	129	AlaAspGluProGlyValLeuGlyArgAspGluLaArgProGlyAlaGluAlaAla	148	
Dd	31	CGAGCTCATCTTGGACGACCTGGGCTGGACGCAGCCGA	--GGGCCGTGGCCGCGTG	87
QY	149	ProSerArgArg-TrrLeuGluArgMetArgArgThrPheGlucluprProThrserser	168	
Dd	88	CCAGAAGTCGCTCTGG-----AACTTCGTGGAGAAGCCGAGTCGTCGTG	132	
QY	168	uaLaalAGlnIleLeuAlaSerValserValVaIPheValIleValserMetValVallie	188	
Dd	133	CCCGCGCGGGTGGGGCGTCTCCTCTCTCTCATCTCTGTCTCTGTCGTGGTGTAT	192	
QY	188	uCysAlaSerThrLeuProAspTrpArgASnAlaAlaAasp----	AsnArgSerLeuAs	207
Dd	193	GTGCATGGGCACCATCCCGAGCTGCAGTGTCTGGACGCGAGGGCAACCGCTGGAGCA	252	
QY	207	pASPArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVa	227	
Dd	253	CCCGACGCTGGAGAGTGGAGCGGTGCATTGGCTGGTTCACCTGGAGTAGCTGTCT	312	
QY	227	IargPherIeValserIlysAsnLysCysGluPheValIysArgProLeuAsnIleIleAs	247	
Dd	313	GGCGCTCTTCGTACCACCAACAAGCTGCATTCGCGCTGCTCTTCATGAACATGTGGA	372	
QY	247	pLeuLeuAlaIleThrProTyrrIleSerValLeuMetThrValPheThrGlyCluAs	267	
Dd	373	CGTGTGGCCATCTCCCTCTTCAAGTAGGCTCACGCTCACACACTGGGTGGCCGCAT	432	
QY	267	nSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTr	287	
Dd	433	GATGAGGTGCACCAACGTGCAGACGGCGTGCAGGCGCTGCGGANTCATGCGCATCGCGG	492	
QY	287	pValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysAr	307	
Dd	493	CATCTTCAAGTGGCCCGCCACTCTCTGGGCGCTGCAGACCTCATCATATGCCCTCAAAGG	552	
QY	307	gCysTyrrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSe	327	
Dd	553	CAGCTTCAAGNAACTGGGGCTGTGCTCATGTACCTGGCAGTGGGTATCTTCTGTCTTCT	612	
QY	327	rAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp----	345	
Dd	613	TGCCCTG-----GGCTACACGTGAGCAGAGCCATCCAGACACCT	654	
QY	346	-PheThrSertileProAlaCysTrpTrpValIleIleSerMetThrThrValGlyTY	365	
Dd	655	GTTTAAGAGCATCCCGAGTCTTCTTGGTGGGCGCATCATCACCATGACCACCGTCGGCTA	714	
QY	365	-rGlyAspMetTyrrProIleThrValProGlyArgIleLeuGlyGlyValCysValIleSe	385	
Dd	715	CGCGACATCTACCCCAGACCCAGCTGGGCAAGCTCAACGGGGCCCATCAGCTTCTTGG	774	
QY	385	-rGlyLeValLeuLeuAlaLeuProIleThrPheIleTyrrHisSerPheValGlnCysTy	405	
Dd	775	TGGTGTATCGCCATCGCCCTGCCCATCCACCCCATCATCAACAACACTTGTTCAGGTACTA	834	
QY	405	rHisGlnLeuLysPheArgSerAlaArgTyrrSerArgSerSerThrGluPheLeuAs	425	
Dd	835	CAACNAGCAGCGCTCTCTGGAGACCGCGGCCAACAGCAGAGCTGGAGCTGATGGAACTCAA	894	
QY	425	n	425	
Dd	895	C	895	

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2004, 10:49:58 ; Search time 3475 Seconds  
(without alignments)  
3652.209 Million cell updates/sec

Title: US-10-016-647-2  
Perfect score: 2215  
Sequence: 1 MTFGSGAASVVLNVGGARY.....HELKFRSARYSRSLSTFLN 425

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -MODEL=frame; p2n.model -DEV=xlh  
-Q/cgn2\_1/USPTO\_spo01/US10016647/runat 19042004 104946 10083/app\_query.fasta\_1.583  
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-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10016647 @CGN 1 1 3437 runat 19042004 104946 10083 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
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2: em\_esthum:\*  
3: em\_estin:\*  
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7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
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15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
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21: em\_gss\_fun:\*  
22: em\_gss\_nam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gsl1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1189	53.7	971	29	CNS0206W	AL175217 Tetraodon
2	916	41.4	772	13	BU274588	BU274588 603533001
3	887	40.0	523	9	AI043703	AI043703 UI-R-CO-1
4	838	37.8	509	29	CG639652	CG639652 OST371309
5	779.5	35.2	2585	29	AY417318	AY417318 Homo sapi
6	777.5	35.1	2582	29	AY417320	AY417320 Mus muscu
7	757	34.2	484	29	CG662016	CG662016 OST444129
8	730	33.0	500	28	AQ02619	AQ02619 HS_5066_A
9	718.5	32.4	2757	11	AK012275	AK012275 Mus muscu
10	718.5	32.4	4390	11	AK034091	AK034091 Mus muscu
11	705	31.8	1857	11	AK076120	AK076120 Mus muscu
12	697	31.5	2936	11	AK046054	AK046054 Mus muscu
13	696	31.4	1476	29	AY415319	AY415319 Mus muscu
14	692.5	31.3	1503	29	AY398781	AY398781 Homo sapi
15	691	31.2	1406	29	AY398783	AY398783 Mus muscu
16	686	31.0	2360	11	AK087481	AK087481 Mus muscu
17	686	31.0	4111	11	AK048819	AK048819 Mus muscu
18	685	30.9	1476	29	AY415317	AY415317 Homo sapi
19	679.5	30.7	1503	29	AY398782	AY398782 Pan trogl
20	666.5	30.1	487	29	CG582101	CG582101 OST222985
21	649.5	29.3	652	12	BJ495239	BJ495239 BJ495239
22	625	28.2	5137	11	BC046490	BC046490 Mus muscu
23	620	28.0	1028	29	CNS04RK5	AL303998 Tetraodon
24	596	26.9	1488	29	AY412413	AY412413 Homo sapi
25	596	26.9	1488	29	AY412415	AY412415 Mus muscu
26	596	26.9	4030	11	AK039559	AK039559 Mus muscu
27	594.5	26.8	1758	29	AY398826	AY398826 Homo sapi
28	593.5	26.8	1758	29	AY398828	AY398828 Mus muscu
29	593.5	26.8	2146	11	BC023222	BC023222 Mus muscu
30	576.5	26.0	505	29	FR0020615	AL013498 F.rubripe
31	574.5	25.9	1572	29	AY400869	AY400869 Homo sapi
32	574.5	25.9	1587	29	AY400871	AY400871 Mus muscu
33	571.5	25.8	1965	29	AY412973	AY412973 Mus muscu
34	571.5	25.8	4780	11	AK036112	AK036112 Mus muscu
35	566	25.6	2946	11	AK045425	AK045425 Mus muscu
36	566	25.6	3458	11	AK044342	AK044342 Mus muscu
37	565.5	25.5	1956	29	AY408065	AY408065 Mus muscu
38	563.5	25.4	1284	29	AY412414	AY412414 Pan trogl
39	563.5	25.4	1944	29	AY408063	AY408063 Homo sapi
40	563.5	25.4	1962	29	AY412971	AY412971 Homo sapi
41	555	25.1	1893	29	AY406812	AY406812 Homo sapi
42	552	24.9	1893	29	AY406814	AY406814 Mus muscu
43	552	24.9	2997	11	AK032268	AK032268 Mus muscu
44	545	24.6	1911	29	AY419307	AY419307 Homo sapi
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# ALIGNMENTS

RESULT 1  
CNS0206W  
LOCUS  
DEFINITION  
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sequence.  
ACCESSION  
AL175217  
VERSION  
AL175217.1  
KEYWORDS  
GSS: genome survey sequence.  
SOURCE  
Tetraodon nigroviridis  
ORGANISM  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontoidea; Tetraodontidae; Tetraodon.

## REFERENCE

## AUTHORS

Roest Crolius H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C.,  
Bernot, A., Fzames, C., Wincker, P., Brotier, P., Quetier, F.,  
Saurin, W., and Weissenbach, J.  
Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)

## JOURNAL

## MEDLINE

## FUBMED

## REFERENCE

## AUTHORS

Roest Crolius H., Jallou, O., Dasilva, C., Ozouf-Costaz, C.,  
Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
Saurin, W., Bernot, A., and Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

## JOURNAL

## MEDLINE

## FUBMED

## REFERENCE

## AUTHORS

Roest Crolius H., Jallou, O., Dasilva, C., Ozouf-Costaz, C.,  
Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
Saurin, W., Bernot, A., and Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

## COMMENT

This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetraodon.

## FEATURES

## source

## Location/Qualifiers

## 1..971

## /organism="Tetraodon nigroviridis"

## /mol\_type="genomic DNA"

## /db\_xref="taxon:99883"

## /clone="221K08"

## /clone\_lib="G"

## /notes="Genoscope sequence ID : C0AG221D04LPI-end : T7"

## ORIGIN

Alignment Scores:  
Prod. No.: 5,78e-122 Length: 971  
Score: 1189.00 Matches: 222  
Percent Similarity: 79.76% Conservative: 32  
Best Local Similarity: 70.09% Mismatches: 38  
Query Match: 53.68% Indels: 30  
DB: 29 Gaps: 4

US-10-016-647-2 (1-425) x CNS0205W (1-971)

82 LysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrp 101  
:::|||||  
8 AGCTCGCTTCTGCTGCTCCTACATGTCGAGCTGCTCTTACACGAGATGCTCTACTGG 67  
:::|||||  
102 GlyLeuGluGluAlaHisLeuGluTyrCysGlnArgLeuAspArgMetSer 121  
:::|||||  
68 GGTCTGAGAGCCGACCTCAGCCGCTGCTCCACGCGCTGAGACCGCTCTGYC 127  
:::|||||  
122 AspThrTyrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArg 141  
:::|||||  
128 GACTGCTTCTGCTCCTCTCTCCGAGGAG-----GAG 160  
:::|||||  
142 ProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgThrPhe 161  
:::|||||  
161 CCGCGGGTCCCGAG--GAGCCAGAGCCGCTGATGAGCGCTTAGGCTGACCTT 217  
:::|||||  
162 GluGluProThrSerSerLeuAlaGlnIleLeuAlaSerValSerValPheVal 181  
:::|||||  
218 GAAGAACCCACCTCGTCACTGGCAGCGCAGATCTGGCTTCTGCTGCTGTTTGTG 277  
:::|||||  
182 IleValSerMetValValLeuGluCysAlaSerThrLeuProAspTyrArgAsnAla----- 199  
:::|||||  
278 GTCTCTCCATGTGATGCTCTGTGCAGACCTTCCGCGAGCTGGAAGACTCCGAGACC 337  
:::|||||

200 -----AlaAlaAspAsnArgSerLeuAsp----- 207  
338 CTGGACCAGCACAGGTAGGTGGTGGGGGGGAGCTGTGTAGAGGTCTGGGGCTCT 397  
208 -----AspArgSerArgIleGluAlaIleCysIleGlyTyrPheThr 222  
398 CTCTGATTGGCGGCTCTCC-TCCAGATCATCGAGACTGTGTGATCAGCTGGTTCACC 456  
223 AlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgPro 242  
457 GCCGAGTGTATGTTCCGGTTCCTGGTGGCGGGGACAAGTGCAGATTGTGCCCGGCT 516  
243 LeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMetThrVal 262  
517 CTGAACATCATCGACCTCTGGCCATCATCCCTTACTAGCTCTCCGTCCGTCACCGACG 576  
263 PheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuMet 282  
577 CTGACGGGGGAAAACTCCAGCTGCAGCGCGGGGTGACCTCCGAGTGTCCGATC 636  
283 MetArgIlePheTyrValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGly 302  
637 ATGAGGATCTTCTGGGTCATCAAGCTAGCGCGTCACTTCTGGGCTTGCAGACGCTCGG 696  
303 LeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAla 322  
697 CTGACGCTTCGACGCTCTACCGGAAATGATGATGCTCTGCTGCTTCTCATCTCGTTGCC 756  
323 MetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSer 342  
757 ATGCGCATCTTCAGTGCACCTGGCAGCTGCTGGACGCGCTCGACCTCGAAGCGGGA 816  
343 AsnLysAspPheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThr 362  
817 AACGAGACTACGCCAGCTCCCGCAGCTGTTGGTGGTGCATCATCTCCATGACGACG 876  
363 ValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCys 382  
877 GTGGGCTACGCGGACATGTACCGGTGACGCGGCGGCGGCTGCTGGCGGCTGTGC 936  
383 ValValSerGlyIleValLeuLeuAlaLeuPro 393  
937 GTTGTGAGCGGATCTGCTGCTGGCGCTGCC 969  
RESULT 2  
BU274588  
LOCUS  
DEFINITION BU274588 772 bp mRNA linear EST 26-NOV-2002  
603533001F1 CS5QCHN53 Gallus gallus cdna clone ChEST490a2 5', mRNA  
sequence.  
ACCSSION  
VERSION BU274588.1 GI:25545538  
KEYWORDS  
EST.  
SOURCE  
ORGANISM Gallus gallus (chicken)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 772)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
MEDLINE  
PUBMED 12443392  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

## Location/Qualifiers

1..772  
/organism="Callus gallus"  
/mol\_type="mRNA"  
/strain="Compton line 151"  
/db\_xref="taxon:9031"  
/clone="ChSRT490a2"  
/sex="Female"  
/tissue\_type="cerebrum"  
/dev\_stage="adult"  
/lab\_host="DHI08"  
/clone\_lib="CSEQCHN53"  
/note="Organ: brain; Vector: pbluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pbluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Alignment Scores:  
Pred. No.: 1,54e-91 Length: 772  
Score: 946.00 Matches: 210  
Percent Similarity: 87.11% Conservative: 13  
Best Local Similarity: 82.03% Mismatches: 13  
Query Match: 41.35% Indels: 23  
DB: 13 Gaps: 4

US-10-016-647-2 (1-425) x BU274588 (1-772)

QY 178 ValValPheValLeuValSerMetValValLeuValCysAlaSerThrLeuProAspTrpArg 197  
Db 5 ATCTCTTCGTATCGTGTGTC-ATGGTGTGTGCTGTGGCCAGCACCCTGCCAGTGGCGG 63  
QY 198 AsnAlaAlaAspAsnArgSerLeuAspArgSerArg----- 211  
Db 64 GC-GCCGGA-----AACCGCAGCTGGAGGAGCAGCAGGATACACACAGTCAGTG 116  
QY 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIle 226  
Db 117 AGGGAGCCCTCAGGGATAATTGAAGCTATCTGCATAGGCTGGTTCACTGCAGATGCATT 176  
QY 227 ValArgPheIleValSerIleValSerIleValSerIleValSerIleValSerIleVal 246  
Db 177 GTGAGGTTTCATCGTTTCAAAGAACAAAGTGTGAGTTTGTGAGAGACCTCTCAACATTAT 236  
QY 247 AspLeuLeuAlaIleThrProTyrTrpIleSerValLeuMetThrValPheThrGlyGlu 266  
Db 237 GATTTACTGGCAATTACTCTTACTACATCTCGTTCTAATGACAGTTTTACAGGGGAA 296  
QY 267 AsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePhe 286  
Db 297 AATTGCACTCCAGAGGGGTGGAGTCACTTTGAGGGTCTTAAAGATGATGAGGA--TTT 354  
QY 287 TrpValIleLeuValLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLys 306  
Db 355 TGGGTGATTAATCGGCTCGTCTATTTCATTTGGCTTCAACACTTGGTCTGACTCTGAAG 414  
QY 307 ArgCysTrpArgGluMetValMetLeuValPheIleCysValAlaMetAlaIlePhe 326  
Db 415 CGTTGTTCACAGAGATGGTGTGCTCTTCTTATCTGTTCTGCTATGCAATTTTC 474  
QY 327 SerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPhe 346  
Db 475 AGTGCACTTTCCAGCTGCTTGAATAAGGGCTGGACTTGGGAACAAGATAGGATTAT 534

## QY

347 ThrSerIleProAlaAlaCysTrpTrpValIleIleSer-MetThrThrValGlyTrpGlu 366  
Db 535 GCCAGCATCCCTGCTGCTGTTGGTGGTGATCATCTCTCATGCCACACAGTGTGTTACGG 594  
QY 366 YAspMetTrpProIleThrValProGlyArg----IleLeuGlyGlyValCysVal-Val 385  
Db 595 TGACATGTGTCCCATCACAGTACCGGAAAGGGATCTTGGAGGGGAATCTGCGTGGGTGA 654  
QY 385 erGlyIleValLeuLeuAlaLeuProIleThr---PheIleTyrHisSerPheValGlnC 404  
Db 655 GTGGCATCGTTTACTAGACCTTGGCCAAATCACCTTTCATTTATCATAGCTTTTGGCAGT 714  
QY 404 ysfYr-HisGlu-LeuLysPheArg-SerAlaArgTyr 415  
Db 715 GTTACCATGAGGCTCAAGTTCGGGATCTGCTAGGTAT 752

## RESULT 3

AI043703

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 523)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Oligo-dT track not found. Not 1 site shown in beginning of sequence

is likely internal to the message. cDNA Library Preparation: M.

Fatima Bonaldo, Ph.D. Clone distribution: clones will be available

through Research Genetics. This clone is also available through the

I.M.A.G.E. Consortium at LNL (info@image.llnl.gov). IMAGE

ID=1783128

Seg primer: M13 Forward

POLYA=No

Location/Qualifiers

1..523

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-CO-31-g-04-0-UI"

/dev\_stage="adult"

/lab\_host="DHI08 (Life Technologies)"

/clone\_lib="UI-R-CO"

/note="Vector: pTrp3b-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO

library is a subtracted library derived from the UI-R-A1

and UI-R-E1 libraries. The UI-R-A1 library consisted of a

mixture of individually tagged normalized libraries

constructed from rat placenta, adult lung, brain, liver,

kidney, heart, spleen, ovary, and muscle. The UI-R-E1

library consisted of a mixture of individually tagged

normalized libraries constructed from 8, 12 and 18-day

embryo. The tag is a string of 3-5 nucleotides present

between the Not I site and the oligo-dT track which



allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)".

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,4e-88 Length: 523  
 Score: 887.00 Matches: 172  
 Percent Similarity: 99.42% Conservative: 0  
 Best Local Similarity: 99.42% Mismatches: 1  
 Query Match: 40.05% Indels: 0  
 DB: 9 Gaps: 0

US-10-016-647-2 (1-425) x AF043703 (1-523)

QY 200 AlaAlaAspAsnArgSerLeuAspArgSerArgileileGluAlaileCysileGly 219  
 Db 3 GCGCCGACAAACGCGAGTCTGGATGACCGGAGGAGGATTAATGAGCTATCTGCAATGAGC 62  
 QY 220 TrpPheThrAlaGluCysileValArgPheileValSerIysAsnIysCysGluPheVal 239  
 Db 63 TGGTTACCCGCGAGTGCATCGTGGGTTTCATCGTCTCCAAAACAAGTGTGAGTTGTC 122  
 QY 240 LysArgProLeuAsnIleileAspLeuLeuAlaileThrProTyrTyrIleSerValLeu 259  
 Db 123 AAGAGACCCCTGACATCATCTGACTTACTGGCAATCACCCCTTATACATCTCCGGTGC 182  
 QY 260 MetThrValPheThrGlyGluAsnSerGlnLeuGluArgAlaGlyValThrLeuArgVal 279  
 Db 183 ATGACAGTGTTCACGCGAGAACTCTCAACTCCAGAGGGCTGGGTCACCCCTGAGGTC 242  
 QY 280 LeuArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheileGlyLeuGln 299  
 Db 243 CTCGGAATGATGGGATCTTCGGGTGATTAAAGCTTGCCTGGCAGTTCATCGGCTGCAG 302  
 QY 300 ThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheile 319  
 Db 303 ACCCTGGGCTTGACTCTCAAGCGATGCTACCGAGAGATGGTATGTGTCTGTCTTCATC 362  
 QY 320 CysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeu 339  
 Db 363 TGTGTGCTATGGGATCTTCAGTGCATCTCTCAGCTCCTTGAGCAGCGGTGGACTTG 422  
 QY 340 GluThrSerAsnIysAspPheThrSerIleProAlaAlaCysThrTrpValIleIleSer 359  
 Db 423 GAGAGTCCAAACAGACITTCACGATCCCGCTGCTGCTGGGTGGTATTATCTCT 482  
 QY 360 MetThrThrValGlyTyrGlyAspMetTyrProIleThr 372  
 Db 483 ATGACTACAGTGGGCTATGGAGACATGTATCTCTCATCA 521

## RESULT 4

CG639652 509 bp DNA linear GSS 02-OCT-2003  
 LOCUS OST371309 Mus musculus 129SV/Ev Mus musculus genomic clone  
 DEFINITION OST371309, genomic survey sequence.  
 ACCESSION CG639652  
 VERSION CG639652.1 GI:37463501  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 509)

REFERENCE  
AUTHORS

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
 Piggett, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
 Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
 Zhu, Q., Person, C. and Sands, A.T.

## TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

## JOURNAL

## COMMENT

Contact: Zambrowicz BP

## OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1..509

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="129SV/Ev"

/db\_xref="taxon:10090"

/clone="OST371309"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129SV/Ev"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.14e-83 Length: 509  
 Score: 838.00 Matches: 164  
 Percent Similarity: 98.20% Conservative: 0  
 Best Local Similarity: 98.20% Mismatches: 2  
 Query Match: 37.83% Indels: 1  
 DB: 29 Gaps: 0

US-10-016-647-2 (1-425) x CG639652 (1-509)

QY 211 ArgIleileGluAlaileCysileGlyTrpPheThrAlaGluCysileValArgPheile 230  
 Db 5 AGGATAATTGAAGTATCTGCATAGGTGTTCCCGGAGTGCATCGTGGCTTCATC 64  
 QY 231 ValSerIysAsnIysCysGluPheValIysArgProLeuAsnIleileAspLeuLeuAla 250  
 Db 65 GTCTCCAAAACAAGTGTGAGTTGTTCAGAGAGCCCTGACATCATTTGACTTACTGGCA 124  
 QY 251 IleThr-ProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLe 270  
 Db 125 ATCAGACCCCTATTACATCTCTGTGCTAATGACAGTGTTCACAGGCGAGAACTCTCAACT 184  
 QY 270 uGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheThrValIleLy 290  
 Db 185 CCAGAGGCGTGGGTGCACCTTGAGGTCCTCCGATGATCGGATCTTCGGGTGATCAA 244  
 QY 290 sLeuAlaArgHisPheileGlyLeuGlnThrLeuGlyLeuThrLysArgCysTyrAr 310  
 Db 245 GCTTGCCCGGCACCTTCATTGGTCTGCAGACACATGGGCTTGACTCTCAAGCGGTGCTACCG 304  
 QY 310 gGluMetValMetLeuLeuValPheileCysValAlaMetAlaIlePheSerAlaLeuSe 330  
 Db 305 AGATGGTATGATGTTACTTGTCTTCATCTGTGTGCTGATGCAATCTTTAGTGCATCTC 364  
 QY 330 rGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnIysAspPheThrSerIlePr 350  
 Db 365 TCAGCTCTTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGATTTGCCAGCATCCC 424  
 QY 350 cAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrPr 370  
 Db 425 CGCTGCTGCTGGGTGATTTATCTATGACTACAGTTGGCTGAGATATGATATCC 484

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QY 370 orleThrValProGlyArg 376
Db 485 TATCAGCGCGCTGGAAGA 503

RESULT 5
AY417318 2565 bp DNA linear GSS 17-DEC-2003
LOCUS Homo sapiens KCNB1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY417318
VERSION AY417318.1 GI:39773278
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2565)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trices
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2565)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
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gene
ORIGIN
Alignment Scores: 2,46e-75 Length: 2565
Pred. No.: 779.50 Matches: 172
Score: 779.50 Conservatives: 82
Percent Similarity: 59.76% Mismatches: 161
Best Local Similarity: 40.47% Indels: 12
Query Match: 35.19% Gaps: 5
DB: 29

US-10-016-647-2 (1-425) x AY417318 (1-2565)
QY 1 MetThrPheGlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAla 18
Db 49 ATGAGAGTCGTGGCGACCAAGGGGTGCTCTCGGGGGTCCGCTCAACGTCGGGGGGCTG 108
QY 19 ArgTyrSerLeuSerArgGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 38
Db 109 CGCGACGAGGTACTCTGGCTACCTGGACCGCTGCCCGCGACGGCTGGCGCAAGCTC 168
QY 39 HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58
Db 169 CGCGACTGCAACACGCGACGACTCGCTCTCGAGGTGTGGATGACTACAGCTTCGACGAC 228
QY 59 AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArg 78
Db 229 AACGAGTACTTCTTGACCGCCACCGCGCGCTTACCTCCATCTCCATCTCTACCGC 288
QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98

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RESULT 6  
AY417320  
LOCUS

AY417320 2562 bp DNA linear GSS 17-DEC-2003

DEFINITION Mus musculus KCB1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417320  
VERSION AY417320.1 GI:39773280  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2562)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1. 2562  
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/mol\_type="genomic DNA"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 4,11e-75 Length: 2562  
Score: 777.50 Matches: 175  
Percent Similarity: 59.77% Conservative: 82  
Best Local Similarity: 40.70% Mismatches: 153  
Query Match: 35.10% Indels: 23  
DB: 29 Gaps: 7  
US-10-016-647-2 (1-425) x AY417320 (1-2562)  
Qy 1 MetThrPheGlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAla 18  
Db 49 ATGGAGATCGTGGCAGCAAGCGGTCTCGCGCGGGTGGCGCTCAACGTGGGGGCCCTG 108  
Qy 19 ArgTySerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeu 38  
Db 109 GCGCAGAGTGTGTGGCGCATCTGACCGCTCGCGCGGTGGCGAGCTC 168  
Qy 39 HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyraArgGluArg 58  
Db 169 CGGAGCTGCAACAGCGAGCATCTCTGCTCCAGTGTGGCAGCATACAGCTCGAGGAC 228  
Qy 59 AsnGluTyrrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrrValArg 78  
Db 229 AAGCAGTACTTCTGCAACCGCCACCTCGCGCGCTTCACCTCTATTCTCAATTCTACCGC 288  
Qy 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyraAsnGluMet 98  
Db 289 ---ACCGCGCGTGCACATGATGGAGAGATGTGCGCTGAGCTTCAGCCAGAGCTG 345  
Qy 99 IleTyrrPheGlyLeuGlyAlaHisLeuGluTyrrCysGlnArgArgLeuAspAsp 118  
Db 346 GACTACTGGGGCATCGATGATGATACCTACCTGGAGTCTGCTGCGAGCGCGCTACCA 405  
Qy 119 ArgMetSerAspThrTyrrThrPheTyrrSerAlaAspGluProGlyValLeu-----Gly 136

Db 406 AAGAA-----GGAGCAGATGAACGAGGAGTGAAGCGGAGGC 443  
Qy 137 ArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArg 156  
Db 444 TGAGACGCTGCGGAGCGGAGCGGCG-AGGAGTTCCGACACACACGTCGTCTGTGAAGA 502  
Qy 157 MetArgArgThrPhe-----GluGluProThrSerSerLeuAlaAlaGlnIleLeu 173  
Db 503 GG-AGAAGACITTTGGGACCTGCTCGAGAGGCCCACTCATCGGTGGCGCCCAAGATCTCTG 561  
Qy 174 AlaSerValSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeu 193  
Db 562 GCATCATCTCCATCATGTCCTCTCCACCATTCGCTCTCACTCAACACACTG 621  
Qy 194 PrcAspTprArgAsnAlaAlaAspAsnArgSerLeuLeuAspAsp---ArgSerArgIle 212  
Db 622 CTTGAGCTACAGAGCTCGAGCAATTCGGCAGAGCAGGACAAACCCGACCTGGCACAC 681  
Qy 213 IleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSer 232  
Db 682 GTGGAGGCTGTGTCATCGCTGGTTCCACCATGAGTACTTGTGAGTTCTCTGTCTCG 741  
Qy 233 LysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThr 252  
Db 742 CCCAAGAATGGAAGTCTTTAAGGCGCCCTCAACGCCATTGACTTACTGGCCATCTCTG 801  
Qy 253 ProTyrrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArg 272  
Db 802 CCTACTAGTCACCATCTCTCTCACAGAATCCAAAGACGCGTGTCTGCTCCAGAT 861  
Qy 273 AlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAla 292  
Db 862 GTGCGCGCTGTGGTCCAGATCTTCGCATCATCGCATCTCTGCGCATCTCTGAAGTTGGCC 921  
Qy 293 ArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrrArgGluMet 312  
Db 922 CGCCACTCCACCGGTCTGAGTCTTGGGCTTCACGCTGGCAGGAGTCAACAGAGCTG 981  
Qy 313 ValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeu 332  
Db 982 GGCTTGCTCATCTCTCTCGCCATGGCATCATGATCTTCTCCAGCTGGTCTTCTTT 1041  
Qy 333 LeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla 352  
Db 1042 GCGAGAGAGATGAGGAT-----GACACCAAGTTCAAAAGCATCCCGCCCTCT 1089  
Qy 353 CysTrpTrpValIleIleSerMetThrThrValGlyTyrrGlyAspMetTyrrProIleThr 372  
Db 1090 TTCTGGTGGGTACCATCACCATGACGCGTGGTTACGAGAGACATCTACCCCTAAGACT 1149  
Qy 373 ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeu 392  
Db 1150 CTCTGGGGAATAATCGTGGGGGCTCTGTGTGATTCGCCGTGCTGTGGTATGGCCCTC 1209  
Qy 393 ProIleThrPheIleTyrrHisSerPheValGlnCysTyrrHisGluLeuLysPheArgSer 412  
Db 1210 CCTTCCTCAATTATCGTCAATAACTTCTCCGAGTTCTCAAGGAGGACAGAGCGCCAGG 1269  
Qy 413 AlaArgTyrrSerArgSerLeuSerThrGlu 422  
Db 1270 AAGCCATCAAGCGGAGAGGCTCTGGAG 1299  
RESULT 7  
CG662016 484 bp DNA linear GSS 02-OCT-2003  
LOCUS OST441129 Mus musculus 129Sv/Ev Mus musculus genomic clone  
DEFINITION OST441129, genomic survey sequence.  
ACCESSION CG662016  
VERSION CG662016.1 GI:37485865  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 484)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Pigott, J., Beltrandeirio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

## FEATURES

Location/Qualifiers

1..484

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="129SV/Ev"

/db\_xref="taxon:10090"

/clone="OST44129"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129SV/Ev"

## ORIGIN

Alignment Scores:

Pred. No.: 4,556-74 Length: 484

Score: 757.00 Matches: 152

Percent Similarity: 95.03% Conservative: 1

Best Local Similarity: 94.41% Mismatches: 6

Query Match: 34.18% Indels: 2

DB: 29 Gaps: 0

US-10-016-647-2 (1-425) x CG662016 (1-484)

QY 211 ArgilleleGluAlaileCysileGlyTTPpPheThrAlaGluCysileValArgPheile 230

Db 5 AGATTAATGAAGTATATCTGATAGGTGGTTCCACGGAGTGCATCGTGGTTCATC 64

QY 231 ValSerIleAsnLysCysGluPheValLysArgProLeuAsnIleleAspLeuAla 250

Db 65 GTCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACATCATTTGGCTTACTGGCA 124

QY 251 IleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeu 270

Db 125 ATCAGCCCTATTACATCTCTGTGCTATGACAGTGTTCACAGCGGAGACCTCACTC 184

QY 271 GlnArgAlaGlyValThrLeuArgValLeuArgMetMet-ArgIlePheTrpVallele 290

Db 185 CAGAGGCTGGGTTCACCTTTGAGGTCTCCGAATGATCGNGGATCTTCTGGGTGATCA 244

QY 290 YLeuAlaArgHisPheileGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrA 310

Db 245 AGCTTGCCCGGCATCTCATTTGGTTCGAGACATGGGCTTGATCTCAACGGGTGTACC 304

QY 310 rGluMetValMetLeuLeuValPheileCysValAlaMetAlailePheSerAlaLeuS 330

Db 305 GAGAGATGGTCACTGTTACTTCTCTCATCTGTGTGTCATGGCAATCTTTTGGCACTCT 364

QY 330 erGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleP 350

Db 365 CTCAGCTCTTGAACATGGGTGGACCTGGAAACATCCAAACAGGATTTCCGACGATCC 424

QY 350 roAlaAlaCysTrpTrpValleleIleSerMetThrThrValGlyTyrGlyAspMetTyr 369

Db 425 CCGCTGCTGCTGGTGGTGGTATCTTATGACTACAGTTGGCTATGGAGATATGCAT 483

## RESULT 8

AQ402619/c

LOCUS

DEFINITION

HS 5066 A2\_E01\_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=642 Col=2 Row=I, genomic survey sequence.

ACCSSION

VERSION

KEYWORDS

SOURCE

AQ402619.1 GI:4413531

GSS.

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 500)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL

MEDLINE

PUBMED

9380589

1049764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 642 row: 1 column: 2

Seq primer: T7

Class: BAC ends

High quality sequence stop: 500.

## FEATURES

Location/Qualifiers

1..500

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/clone="Plate=642 Col=2 Row=I"

/sex="male"

/clone\_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

## ORIGIN

Alignment Scores:

Pred. No.: 5,116-71 Length: 500

Score: 730.00 Matches: 144

Percent Similarity: 93.63% Conservative: 3

Best Local Similarity: 91.72% Mismatches: 10

Query Match: 32.96% Indels: 0

DB: 28 Gaps: 0

US-10-016-647-2 (1-425) x AQ402619 (1-500)

QY 267 AnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePhe 286

Db 498 AACTCTCAACTCCAGAGGCTGAGTCCACCTTGAGGTACTTAGAATGATGAGGATATT 439

QY 287 TrpValIleLysLeuAlaArgHisPheileGlyLeuGlnThrLeuGlyLeuThrLeuLys 306

Db 438 TGGGTGATTAAAGCTTGCAGAGTCACTTCATTTGGTCTTCAGACACTCGGTTTGACTCTCAA 379

QY 307 A-gCysTyrArgGluMetValMetLeuLeuValPheileCysValAlaMetAlailePhe 326













```

QY 63 PheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrrValArgGlyHisGlyLys 82
Db 379 TTTGATCGCAGCTCTCAGGGCTTCGTTATGTCCTGCACACTATCGC---ACTGGTCGC 435
QY 83 LeuArgPheAlaProArgMetCysGluLeuSerPheTyrrAsnGluMetIleTyrrTrpGly 102
Db 436 CTGATGTCATGAGCAGCTCTGTCGCTCTCTCTTTCTTTCAGGAGATCCAGTACTGGGC 495
QY 103 LeuGluGlyAlaHisLeuGluTyrrCysGlnArgArgLeuAspArg-----Met 120
Db 496 ATAGATGAACCTCAGCATTGCTCTGCTGCTGAGGACAGATACTTCCAGAAAGAGAGCTG 555
QY 121 SerAspThrTyrrThrPheTyrrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 556 AGTGAACCTCTGATCTTTAAGAGGACACAGATGACCCAGGAAAGTCAACATGAGTGA 615
QY 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgGThr 160
Db 616 CAGGACTTCTCAAGAGGACCTTGTCCACACTGTCGA-----CAAAAGCTCTGGATAT 669
QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPhe 180
Db 670 CTGAGAAACCTGTGATCTTCACAGCAGCCCGATCTTTGGAGTAATCTCCATCATTTT 729
QY 181 ValIleValSerMetVal-----ValLeuCysAlaSerThrLeuProAspTrpArgAsn 198
Db 730 GTGGCAGTGTCCATCTGTCACATGCGCCTGATGTCAGTGCAGTT---AGCTGGCTCAAC 786
QY 199 AlaAlaAlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIle 218
Db 787 CTA-----CAGCTCTGGAGATCTTGGAGTATGTGTCATC 822
QY 219 GlyTrpPheThrAlaGluCysIleValArgPheIleValSerIysAsnLysCysGluPhe 238
Db 823 AGCTGGTTCACCGGAGTTCGTTCGCTTCTCTATGTGTGAACAGAGTGCACCTTC 882
QY 239 ValIysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrrIleSerVal 258
Db 883 CTGAGGAAGTTCACAAACATCATAGACCTCTTGCATCTTGCCTTCTATATACTCTT 942
QY 259 LeuMetThrValPheThrGlyGluAsnSer-----GlnLeuGlnArgAlaGlyValThr 276
Db 943 CTGGTGAAGCTGAGCGGCACCCACACACAGAGCTGGAATGTGGAGCTGTG 1002
QY 277 LeuArgValLeuArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheIle 296
Db 1003 GTCCAGTCTTGAGGCTCTCAGAGCTCTCGCATGCTGAACTGGGAAGGATCTTACA 1062
QY 297 GlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrrArgGluMetValMetLeuLeu 316
Db 1063 GGATTCGCTCACTTGGGATGACAATCACTCACTGCTGATGATGATGAGAGTTCGCTCT 1122
QY 317 ValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGly 336
Db 1123 CTGTTCTATCTGCGGATTTCTATTTTCAACATGATATCTTCCAGAGCAAGC 1182
QY 337 LeuAspLeuGluThrSerAsnLysAspPheThrIleProAlaAlaCysTrpTrpVal 356
Db 1183 ATTCCTGATACAACC-----TTCAAGTGTTCCTTGTGATGATGGTGGGC 1230
QY 357 IleIleSerMetThrThrValGlyTyrrGlyAspMetTyrrProIleThrValProGlyArg 376
Db 1231 ACACATCTCATGACTACAGTAGATAGGGAATAGCCAGACACACACACAGGCAAA 1290
QY 377 IleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPhe 396
Db 1291 ATGCTGGCCTACATGATGATTTCTGTGAGGAATCTTGTCTGCTTGTGCTTATTCCTT 1350
QY 397 IleTyrrHisSerPheValGlnCysTyrrHisGluLeuLysPheArgSerAla 413
Db 1351 ATTAATGATGATCTCTCTGCTGCTACTCTTACCTTGAACCTCAAGGAAGCA 1401

```

RESULT 12  
AK046054  
LOCUS  
DEFINITION

AK046054 2936 bp mRNA linear HTC 20-SEP-2003  
Mus musculus adult male corpora quadrigemina cDNA, RIKEN  
full-length enriched library, clone:B230338H13  
product:voltage-gated potassium channel alpha chain Kv9.3 homolog  
(Rattus norvegicus), full insert sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AK046054.1 GI:26337794  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636  
2

REFERENCE

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159  
3

REFERENCE

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Izawa, Y., Ozawa, K., Tanaka, T., Matsuda, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multipillar sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4

REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5

REFERENCE

The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2936)

REFERENCE

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

COMMENT

cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.

## FEATURES

source

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1. .2936
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/strain="C57BL/6J"
/db_xref="FANTOM.DB:B230338H13"
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/dev_stage="adult"
441. .1916
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**CDS**

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/!note="unnamed protein product; putative
voltage-gated potassium channel alpha chain Kv9.3 homolog
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DEJVEGIEACIAMVTEGLAIRAPQSKQWKLNIIDFVSIIPRYATLAVDTKE
BESDILNMGKQVGLKLMRIPLRLKARHVSGLSLGRLHVSVEHVGLLLLPSCVL
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## ORIGIN

Alignment Scores:

Pred. No.:	5,48e-66	Length:	2936
Score:	697.00	Matches:	149
Percent Similarity:	55.63%	Conservative:	93
Best Local Similarity:	34.25%	Mismatches:	149
Query Match:	31.47%	Indels:	44
DB:	11	Gaps:	11

US-10-016-647-2 (1-425) X AK046054 (1-2936)

Qy	1	MetThrPheGly-----	ArgSerGlyAlaalaSer-----	ValValValLeu	14
Db	441	ATGGTGTTTGGAGAGT	TTTTCATGCCTCGACAAGATGAGGA	CTTGTCAACTTGTGAAC	500
Qy	15	ValGlyGlyAlaArgTy-Ser	LeuSerArgGluLeuLeuLysAsp	PheProLeuArgArg	34
Db	501	GTTGGGGGGCTTTAAG	CAGTCTGTGGATCAAAAGTAC	CTCTCTGGGTTCCTCACACAGA	560
Qy	35	ValSerArgGluHisGlyCys	ArgSerGluArgaspValLeuGluValCys	AspAspTyr	54
Db	561	CTGGGAAAGCTCTTACT	TGCGACCTCTGAGAGGCCATCTTG	GAGCTGTGTGTGATGATCA	620
Qy	55	AspArgGluArgAsnGluTy	PhePheAspArgHisSerGluAlaPhe	GlyPheLeuLeu	74
Db	621	AGCTGGCAGATAAAGAT	GTATCTTTTCATCGGAACCCCTTC	TGTTTCAGATACAGCTCTTG	680

RESULT 13

AY415319

LOCUS

## DEFINITION

ACCESSION

VERSION \_\_\_\_\_

## KEYWORDS

115	ArgLeu-----	AspAspArgMetSerAsp	121
798	CGGTACAGAGAGCCGAAGAGAGAGAGCCACGACAGGACTGGACACAGAAAGCAACGAT	857	
123	ThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArg-----	137	
858	GTGAGCAGACACTCCTCCTTTGAGAAATCGTCTCTGTTGAGAAGAGACTGGAGAAGTTT	917	
138	AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTyrLeuGluArgMet	157	
918	GATGAGCTGAGATTGTCAGCTCCGA-----AAGAAGATCTGGATTCTGA-----	962	
158	ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnLeuLeuAlaSerValSer	177	
963	-----ATGGAAATCCAGCTTACTGCCTGTGGCGCAAGCTCATTTGCCATCTCCTCC	1013	
178	ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArg	197	
1014	TTGAGCGTGTGTGGTTCATAGTAGGCCATGTGTGTGCACAGCATGTGCGAANTCCAG	1073	
198	AsnAlaAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleLeuAlaIle---	216	
1074	AAC-----GAGGATGAGAAGTGGATGAC-----CCTGTGCTGGAAGGTGTGGAG	1118	
217	-----CysIleGlyTrpPheThrAlaGluCysIleValAlaArgPheIleValSerIysAsn	234	
1119	ATTGCCTGCATTCGATGGTTTACTGTGTGAGCTAGCCATCAGGCTGGTGTCTCTCCATCA	1178	
235	LysCysGluPheValIysArgProLeuAsnIleLeuAspLeuLeuAlaIleThrProTyr	254	
1179	CAAAAGAAGTTCGAAAAACCCCTCTGAACATCATTTGCTTGTCTATCATTCCTCCTTC	1233	
255	TyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnhrgAlaGly	274	
1239	TATGCCACGTTGGGTGGGACACCAAGAGAGAGAGACTGAGGACATTCGAAATATGGGC	1299	
275	ValThrLeuArgValLeuArgMetMetArgIlePheTyrValIleLysLeuAlaArgHis	294	
1299	AAGTGTGTCACAGATCCTTCGGCTCATGAGGATTTCCGAATTCGAACTTGCCTGGCAC	1355	
295	PheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet	314	
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315	LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGlu	334	
1419	CTGCTTCCTCTCTCTGTGGGCACTCCATCTTCTCT-----GTGCTTATC	1466	
335	HisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrp	354	
1467	TACTCTGTGGAGAAAGATGAACACAAGTCCAGTCTCACGACATCCCCATCTGCTGGTGG	1521	
355	TrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValPro	374	
1527	TGGGCCACTATCAGTATGACACACAGTGGGTATGGAGACACCCACCGACGTACCTTAGCT	1581	
375	GlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProfile	394	
1587	GGGAAATCATTCGAACACATGATTATCTGTGGATCTTAGTGTAGCCCTCCCAATT	1641	
395	ThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys	409	
1647	ACCATCATCTTCAACAAGTTTTCGAAGTACTTACCAGAAGCAGAAA	1691	

[illegible]

## RESULT 13

AY415319

## LOCUS

## DEFINITION

ACCESSION

VERSION \_\_\_\_\_

## KEYWORDS

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 1476)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 1476)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 Query Match: 31.42% Indels: 38  
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Db 466 CTGGAGAAGTTTGTAGCTGAGTGGATTTGTGCTCAGCTCCGA-----AAGAAGATCTGG 516  
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 QY 174 AlaserValSerValValPheValIleValSerMetValValLeuCysAlaserThrLeu 193  
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 QY 214 GluAlaIle-----CysIleGlyTyrPheThrAlaGluCysIleValAlaArgPheIle 230  
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 QY 271 GlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTyrValIleLys 290  
 Db 847 GAGAAATATGGCAAGTGGTCCAGATCCTTCGGCTCATGAGGATTTCCGAATTTCTGAAG 906  
 QY 291 LeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLysArgCysTyrArg 310  
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 genomic survey sequence.  
 VERSION AY398781.1 GI:39748569  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1503)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
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 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 TITLE

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1503)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment  
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Pred. No.: 692.50 Matches: 155  
Score: 55.78% Conservative: 91  
Percent Similarity: 35.15% Mismatches: 157  
Best Local Similarity: 31.26% Indels: 39  
Query Match: 29 Gaps: 10  
DB: 10  
US-10-016-647-2 (1-425) x AY398781 (1-1503)  
QY 5 ArgSerGlyAlaAlaSerValLeuAsnValGlyGlyValArgTyrSerLeuSerArg 24  
DB 107 CGTCCGGGACTCTTCACG-GTC-----AACGTGGGGGCGGCTTCGTCTTCGCGAG 162  
QY 25 GluLeuLeuAspPheProLeuArgArgValSerArgLeu----- 38  
DB 163 CAGGCGCTGTCGCTTCGCGACACGCGCTTGGCAAGCTGCGCGTGGTGGCTTC 222  
QY 39 -----HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyr 54  
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QY 55 AspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeu 74  
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QY 95 TyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArg 114  
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DB 460 AGNN 519  
QY 135 LeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeu 154  
DB 520 NNN 579  
QY 155 GluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAla 174  
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DB 640 GTCATCTCCATTATCTTCGTGGTGGTGTCTCCATCATTAACATGCGCTGATGTCAGCTAG 699  
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DB 1201 GACACCCACACAGGCAAAATCGTGGCTTCAATGATATATATATATCGGAAATCTTGTCT 1260  
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DEFINITION Mus musculus KCNv1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY398783  
VERSION AY398783.1 GI:39748571  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1406)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
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REFERENCE 2 (bases 1 to 1406)

